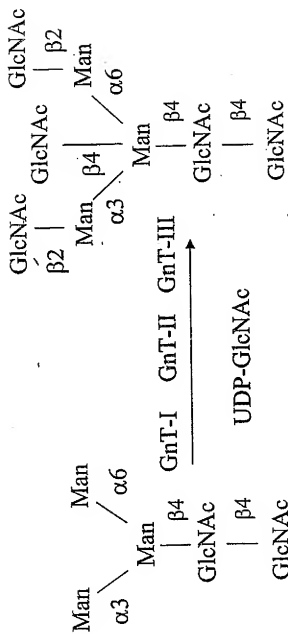


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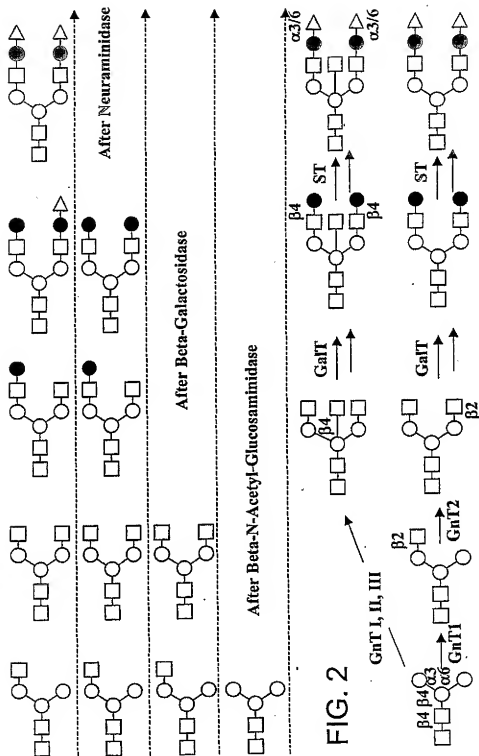


Trimannosyl core with
Bisecting GlcNAc

Trimannosyl core

FIG. 1

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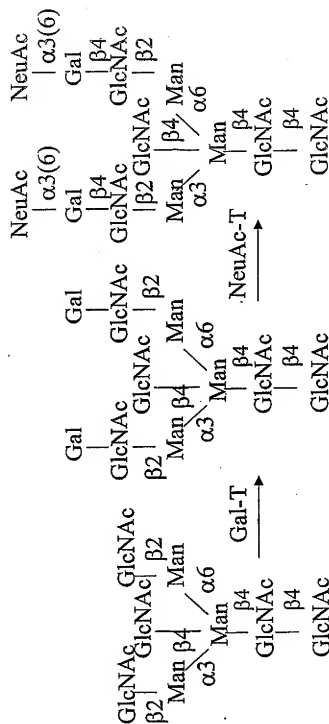


FIG. 3

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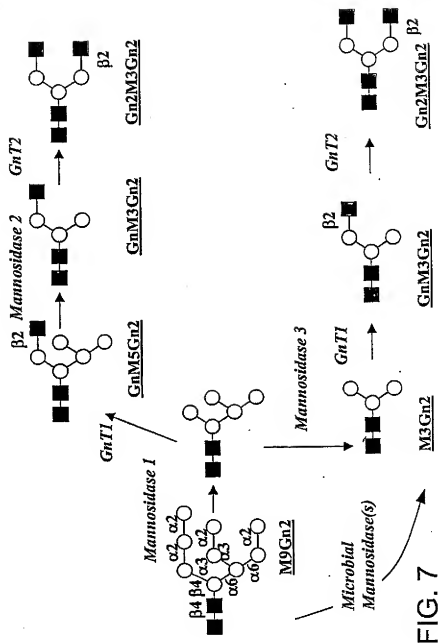


FIG. 7

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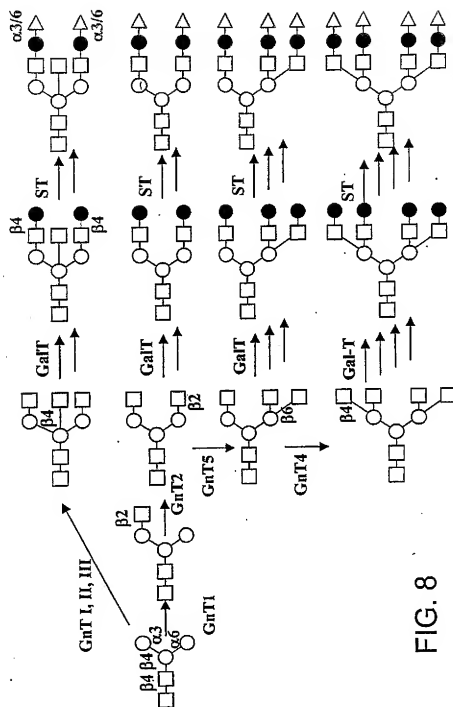


FIG. 8

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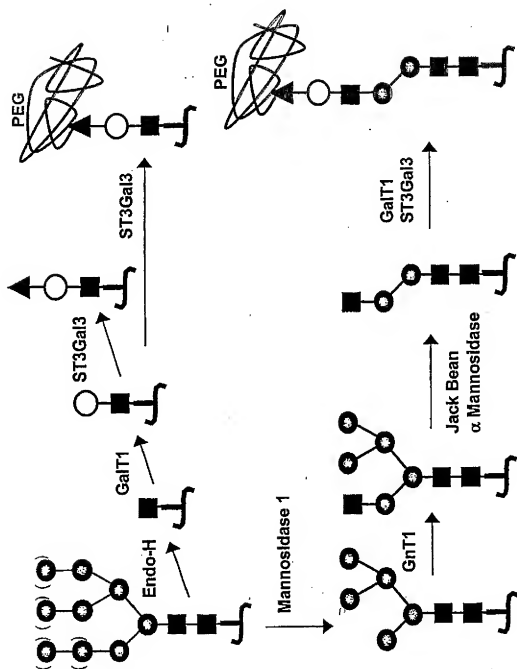


FIG. 9

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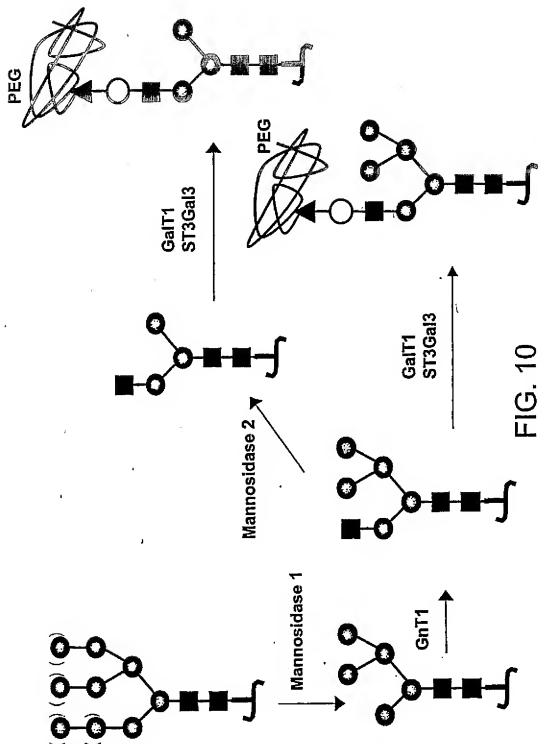


FIG. 10

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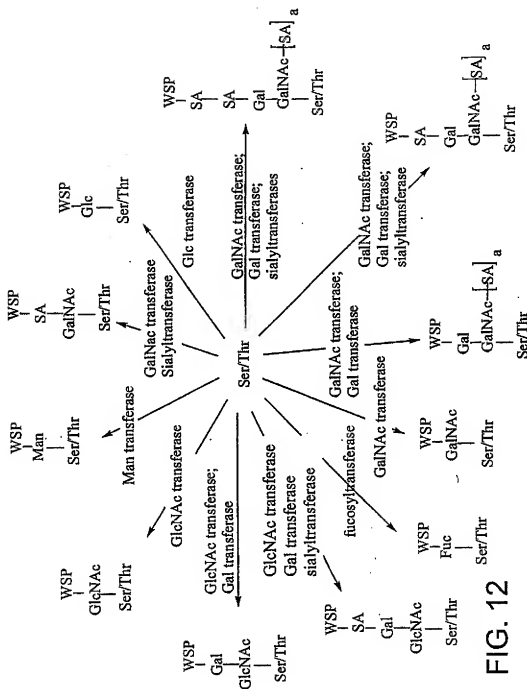


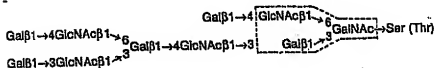
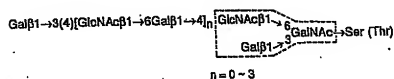
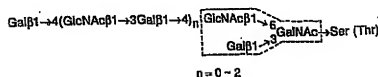
FIG. 12

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Core 1



Core 2



Core 3



Core 4

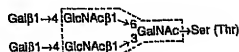


FIG. 13

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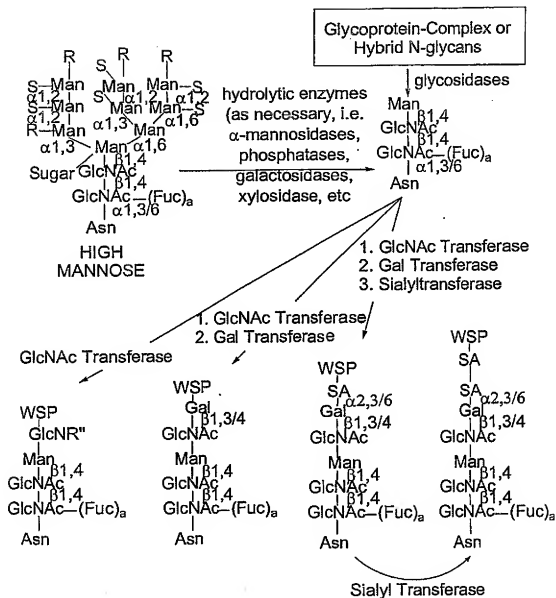


FIG. 15

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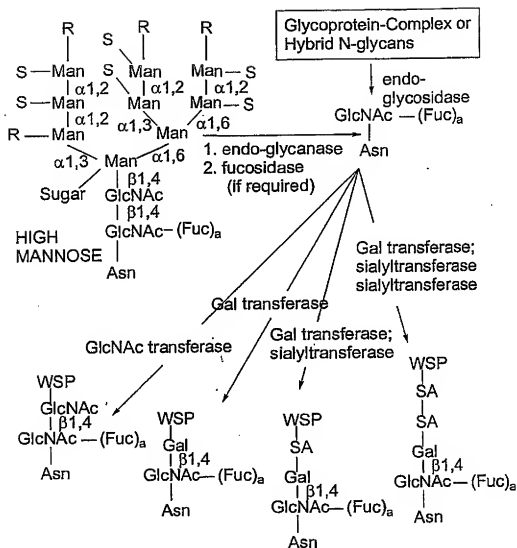


FIG. 17

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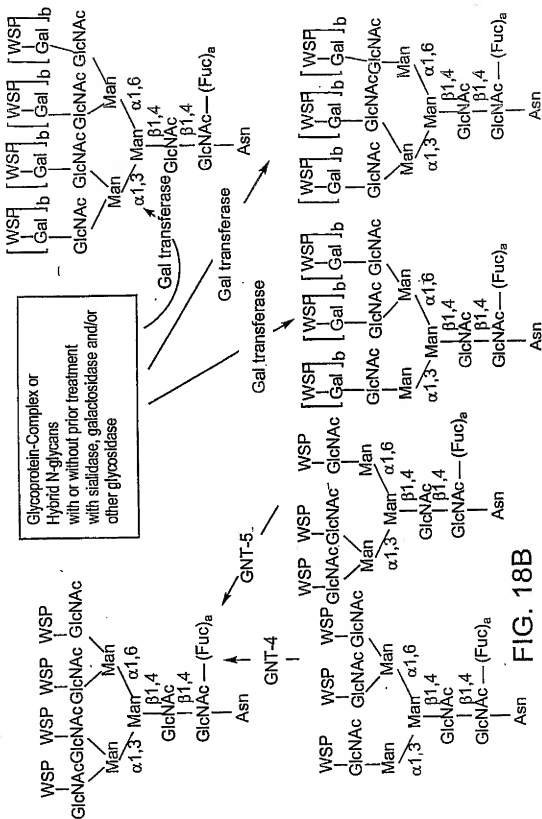


FIG. 18B

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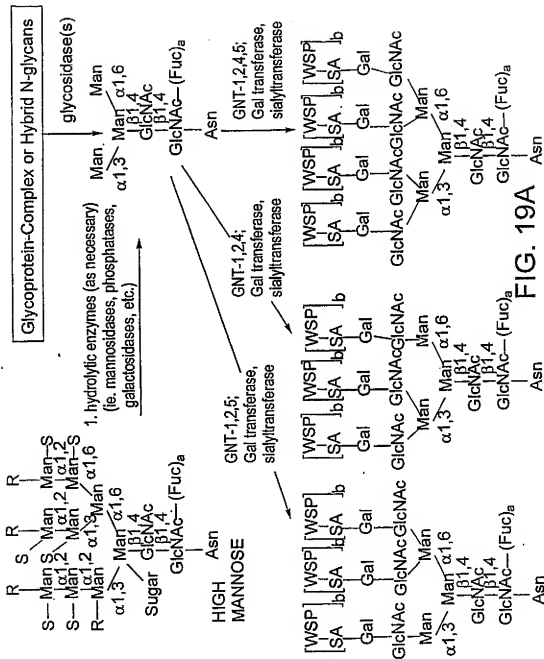
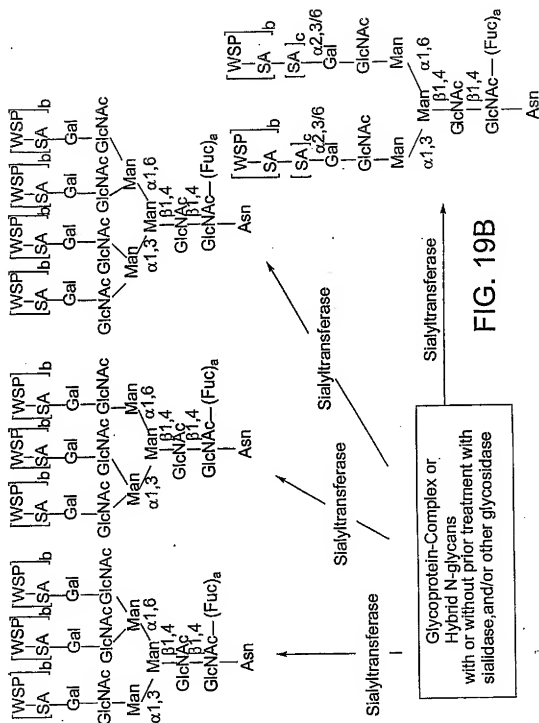


FIG. 19A

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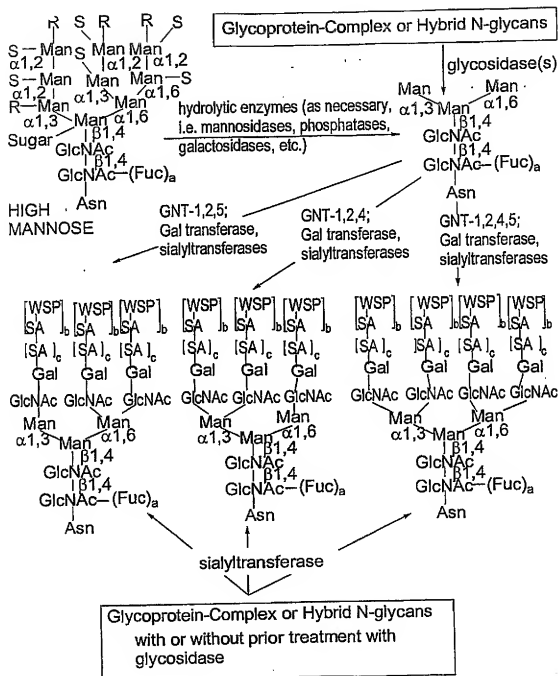


FIG. 20

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O-LINKED OLIGOSACCHARIDES

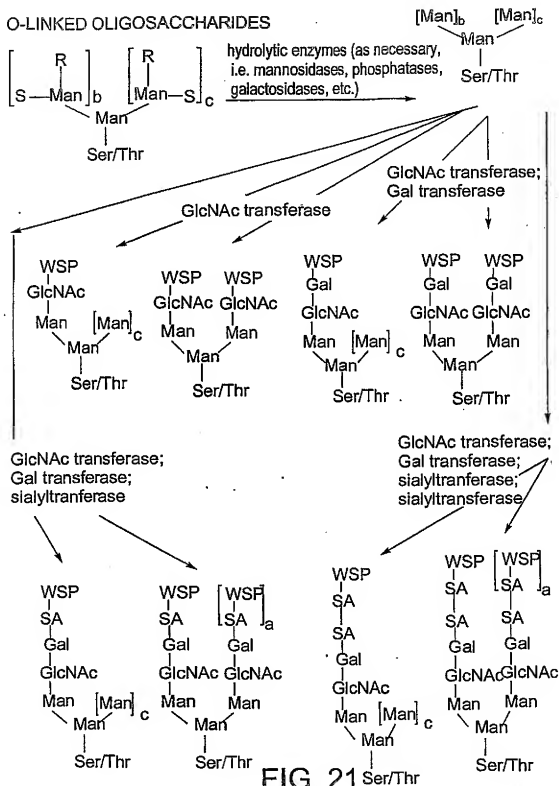


FIG. 21

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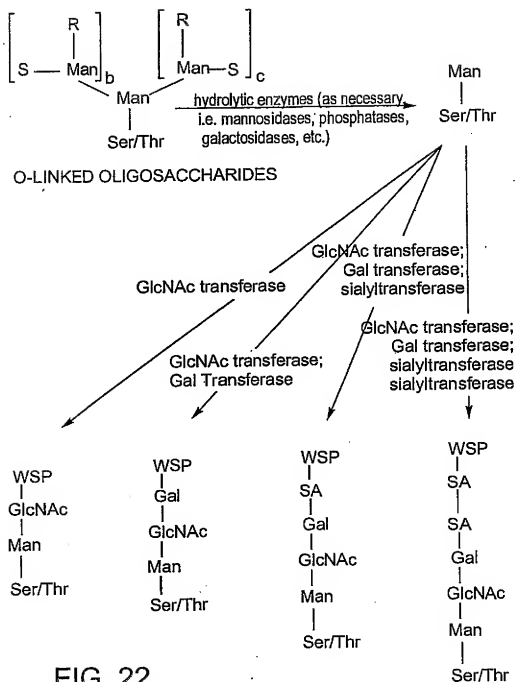


FIG. 22

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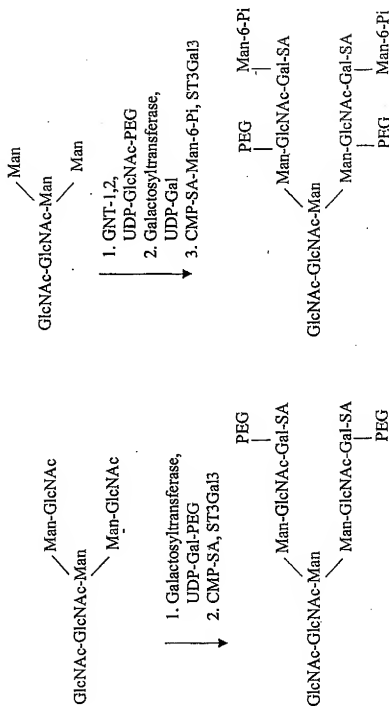


FIG. 23A

FIG. 23B

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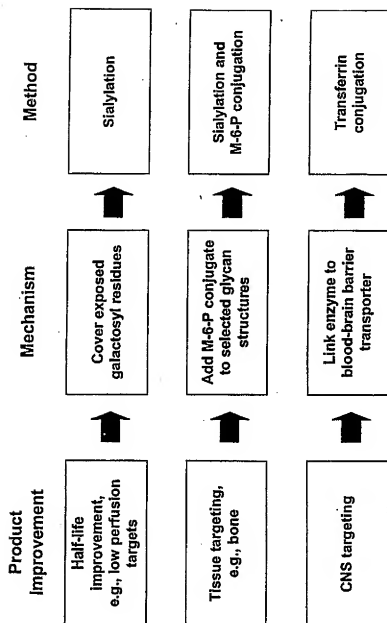


FIG. 24

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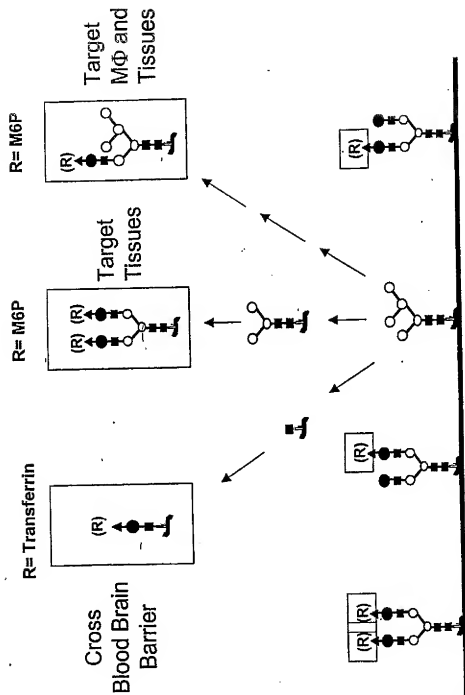


FIG. 25

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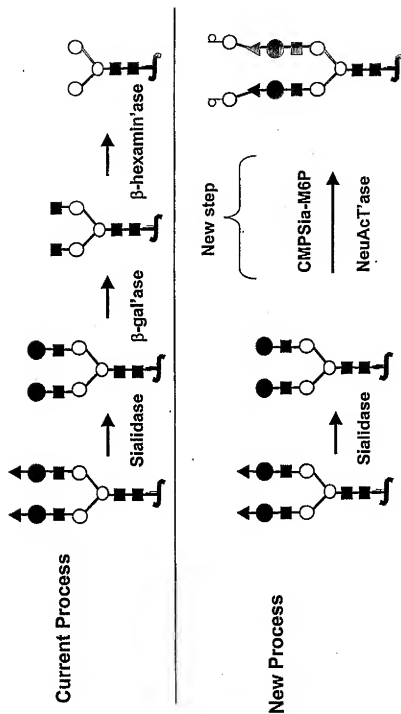


FIG. 26

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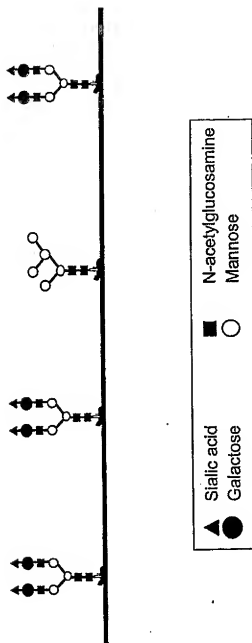


FIG. 27

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12AP1/E5 -- Viventia Biotech
 1964 -- Aventis
 20K growth hormone -- AMUR
 28P6/E6 -- Viventia Biotech
 3-Hydroxyphthaloyl-beta-lactoglobulin --
 4-IBB ligand gene therapy --
 64-Cu MAb conjugate TETA-1A3 --
 Mallinckrodt Institute of Radiology
 64-Cu MAb conjugate TETA-cT84.66
 64-Cu Trastuzumab TETA conjugate --
 Genentech
 A 200 -- Amgen
 A10255 -- Eli Lilly
 A1PDX -- Hedral Therapeutics
 A6 -- Angstrom
 aaAT-III -- Genzyme
 Abciximab -- Centocor
 ABI.001 -- Atlantic BioPharmaceuticals
 ABT-828 -- Abbott
 Accutin
 Actinohivin
 activin -- Biotech Australia, Human
 Therapeutics, Curis
 AD 439 -- Tanox
 AD 519 -- Tanox
 Adalimumab -- Cambridge Antibody Tech.
 Adenocarcinoma vaccine -- Biomira -- NIS
 Adenosine deaminase -- Enzond
 Adenosine A2B receptor antagonists --
 Adenosine Therapeutics
 ADP-001 -- Axis Genetics
 AF 13948 -- Affymax
 Afelimomab -- Knoll
 AFP-SCAN -- Immunomedics
 AG 2195 -- Corixa
 agalsidase alfa -- Transkaryotic Therapies
 agalsidase beta -- Genzyme
 AGENT-- Antisoma
 AI 300 -- AutoImmune
 AI-101 -- Teva
 AI-102 -- Teva
 AI-201 -- AutoImmune
 AI-301 -- AutoImmune
 AIDS vaccine -- ANRS, CIBG, Hesel
 Biomed, Hollis-Eden, Rome, United
 Biomedical, American Home Products,
 Maxygen
 airway receptor ligand -- IC Innovations
 AJvW 2 -- Ajinomoto
 AK 30 NGF -- Alkermes
 Albuferon -- Human Genome Sciences
 albumin -- Biogen, DSM Anti-Infectives,
 Genzyme Transgenics, PPL Therapeutics,
 TranXenoGen, Welfide Corp.
 aldesleukin -- Chiron
 alefacept -- Biogen
 Alemtuzumab
 Allergy therapy -- ALK-Abello/Maxygen,
 ALK-Abello/RP Scherer
 allergy vaccines -- Allergy Therapeutics
 Alnidofibatide -- Aventis Pasteur
 Alnorine -- SRC VB VECTOR
 ALP 242 -- Gruenenthal
 Alpha antitrypsin -- Arriva/Hyland
 Immuno/ProMetic/Protease Sciences
 Alpha-1 antitrypsin -- Cutter, Bayer, PPL
 Therapeutics, Profile, ZymoGenetics,
 Arriva
 Alpha-1 protease inhibitor -- Genzyme
 Transgenics, Welfide Corp.
 Alpha-galactose fusion protein --
 Immunomedics
 Alpha-galactosidase A -- Research
 Corporation Technologies, Genzyme
 Alpha-glucosidase -- Genzyme, Novazyme
 Alpha-lactalbumin
 Alpha-L-iduronidase -- Transkaryotic
 Therapies, BioMarin
 alteplase -- Genentech
 alvircept sudotox -- NIH
 ALX1-11 -- sNPS Pharmaceuticals
 Alzheimer's disease gene therapy

FIG. 28A

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AM-133 -- AMRAD
 Amb a 1 immunostim conj. -- Dynavax
 AMD 3100 -- AnorMED -- NIS
 AMD 3465 -- AnorMED -- NIS
 AMD 3465 -- AnorMED -- NIS
 AMD Fab -- Genentech
 Amediplase -- Menarini, Novartis
 AM-F9
 Amoebiasis vaccine
 Amphiregulin -- Octagene
 anakinra -- Amgen
 analgesic -- Nobex
 anacstim -- Amgen
 AnergiX.RA -- Corixa, Organon
 Angiocidin -- InKine
 angiogenesis inhibitors -- ILEX
 AngioMab -- Antisoma
 Angiopoietins -- Regeneron/Procter & Gamble
 angiotatin -- EntreMed
 Angiostatin/endostatin gene therapy -- Genetix Pharmaceuticals
 angiotensin-II, topical -- Maret
 Anthrax -- EliSys Therapeutics/US Army Medical Research Institute
 Anthrax vaccine
 Anti platelet-derived growth factor D human monoclonal antibodies -- CuraGen
 Anti-17-1A MAb 3622W94 -- GlaxoSmithKline
 Anti-2C4 MAb -- Genentech
 anti-4-1BB monoclonal antibodies -- Bristol-Myers Squibb
 Anti-Adhesion Platform Tech. -- Cytovax
 Anti-adipocyte MAb -- Cambridge Antibody Tech./ObesSys
 antiallergics -- Maxygen
 antiallergy vaccine -- Acambis
 Anti-alpha-4-integrin MAb
 Anti-alpha β 3 integrin MAb -- Applied Molecular Evolution
 Anti-angiogenesis monoclonal antibodies -- KS Biomedix/Schering AG
 Anti-B4 MAb-DC1 conjugate -- ImmunoGen
 Anti-B7 antibody PRIMATIZED -- IDEC
 Anti-B7-1 MAb 16-10A1
 Anti-B7-1 MAb 1G10
 Anti-B7-2 MAb GL-1
 Anti-B7-2-gelonin immunotoxin -- Antibacterials/antifungals -- Diversa/IntraBiotics
 Anti-beta-amyloid monoclonal antibodies -- Cambridge Antibody Tech., Wyeth-Ayerst
 Anti-BLyS antibodies -- Cambridge Antibody Tech./Human Genome Sciences
 Antibody-drug conjugates -- Seattle Genetics/Eos
 Anti-C5 MAb BB5-1 -- Alexion
 Anti-C5 MAb N19-8 -- Alexion
 Anti-C8 MAb
 anticancer cytokines -- BioPulse
 anticancer matrix -- Telios Integra
 Anticancer monoclonal antibodies -- ARIUS, Immunex
 anticancer peptides -- Maxygen, Micrologix
 Anticancer prodrug Tech. -- Alexion
 Antibody Technologies
 anticancer Troy-Bodies -- Affite -- Affitech
 anticancer vaccine -- NIH
 anticancers -- Epimmune
 Anti-CCR5/CXCR4 sheep MAb -- KS Biomedix Holdings
 Anti-CD11a MAb KBA --
 Anti-CD11a MAb M17
 Anti-CD11a MAb TA-3 --
 Anti-CD11a MAb WT.1 --
 Anti-CD11b MAb -- Pharmacia
 Anti-CD11b MAb LM2
 Anti-CD154 MAb -- Biogen
 Anti-CD16-anti-CD30 MAb -- Biotest
 Anti-CD18 MAb -- Pharmacia
 Anti-CD19 MAb B43 --

FIG. 28B

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Anti-CD19 MAb -liposomal sodium butyrate conjugate -	Anti-CD4 MAb 4162W94 - GlaxoSmithKline
Anti-CD147	Anti-CD4 MAb B-F5 - Diaclone
Anti-CD19 MAb-saporin conjugate -	Anti-CD4 MAb GK1-5
Anti-CD19-dsFv-PE38-immunotoxin -	Anti-CD4 MAb KT6
Anti-CD2 MAb 12-15 -	Anti-CD4 MAb OX38
Anti-CD2 MAb B-E2 - Diaclone	Anti-CD4 MAb PAP conjugate - Bristol-Myers Squibb
Anti-CD2 MAb OX34 -	Anti-CD4 MAb RIB 5-2
Anti-CD2 MAb OX54 -	Anti-CD4 MAb W3/25
Anti-CD2 MAb OX55 -	Anti-CD4 MAb YTA 3.1.2
Anti-CD2 MAb RM2-1	Anti-CD4 MAb YTS 177-9
Anti-CD2 MAb RM2-2	Anti-CD40 ligand MAb 5c8 - Biogen
Anti-CD2 MAb RM2-4	Anti-CD40 MAb
Anti-CD20 MAb BCA B20	Anti-CD40 MAb 5D12 - Tanox
Anti-CD20-anti-Fc alpha RI bispecific MAb - Medarex, Tenovus	Anti-CD44 MAb A3D8
Anti-CD22 MAb-saporin-6 complex -	Anti-CD44 MAb GKWA3
Anti-CD3 immunotoxin -	Anti-CD44 MAb IM7
Anti-CD3 MAb 145-2C11 - Pharming	Anti-CD44 MAb KM81
Anti-CD3 MAb CD4IgG conjugate - Genentech	Anti-CD44 variant monoclonal antibodies - Corixa/Hebrew University
Anti-CD3 MAb humanised - Protein Design, RW Johnson	Anti-CD45 MAb BC8-I-131
Anti-CD3 MAb WT32	Anti-CD45RB MAb
Anti-CD3 MAb-ricin-chain-A conjugate -	Anti-CD48 MAb HuLy-m3
Anti-CD3 MAb-xanthine-oxidase conjugate -	Anti-CD48 MAb WM-63
	Anti-CD5 MAb - Becton Dickinson
Anti-CD30 MAb BerH2 - Medac	Anti-CD5 MAb OX19
Anti-CD30 MAb-saporin conjugate	Anti-CD6 MAb
Anti-CD30-scFv-ETA'-immunotoxin	Anti-CD7 MAb-PAP conjugate
Anti-CD38 MAb AT13/5	Anti-CD7 MAb-ricin-chain-A conjugate
Anti-CD38 MAb-saporin conjugate	Anti-CD8 MAb - Amerimmune, Cytodyn, Becton Dickinson
Anti-CD3-anti-CD19 bispecific MAb	Anti-CD8 MAb 2-43
Anti-CD3-anti-EGFR MAb	Anti-CD8 MAb OX8
Anti-CD3-anti-interleukin-2-receptor MAb	Anti-CD80 MAb P16C10 - IDEC
Anti-CD3-anti-MOV18 MAb - Centocor	Anti-CD80 MAb P7C10 - ID Vaccine
Anti-CD3-anti-SCLC bispecific MAb	Anti-CD8-idarubicin conjugate
Anti-CD4 idiotypic vaccine	Anti-CEA MAb CE-25
Anti-CD4 MAb - Centocor, IDEC Pharmaceuticals, Xenova Group	Anti-CEA MAb MN 14 - Immunomedics
Anti-CD4 MAb 16H5	Anti-CEA MAb MN14-PE40 conjugate - Immunomedics

FIG. 28C

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Anti-CEA MAb T84.66-interleukin-2 conjugate
 Anti-CEA sheep MAb -- KS Biomedix Holdings
 Anti-cell surface monoclonal antibodies -- Cambridge Antibody Tech. /Pharmacia
 Anti-c-erbB2-anti-CD3 bifunctional MAb -- Otsuka
 Anti-CMV MAb -- Scotgen
 Anti-complement
 Anti-CTLA-4 MAb
 Anti-EGFR catalytic antibody -- Hesel Biomed
 anti-EGFR immunotoxin -- IVAX
 Anti-EGFR MAb -- Abgenix
 Anti-EGFR MAb 528
 Anti-EGFR MAb KSB 107 -- KS Biomedix
 Anti-EGFR MAb-DM1 conjugate -- ImmunoGen
 Anti-EGFR MAb-LA1 --
 Anti-EGFR sheep MAb -- KS Biomedix
 Anti-FAP MAb F19-I-131
 Anti-Fas IgM MAb CH11
 Anti-Fas MAb Jo2
 Anti-Fas MAb RK-8
 Anti-Fit-1 monoclonal antibodies -- ImClone
 Anti-fungal peptides -- State University of New York
 antifungal tripeptides -- BTG
 anti-ganglioside GD2 antibody-interleukin-2 fusion protein -- Lexigen
 Anti-GM2 MAb -- Kyowa
 Anti-GM-CSF receptor monoclonal antibodies -- AMRAD
 Anti-gp130 MAb -- Tosoh
 Anti-HCA monoclonal antibodies -- AltaRex/Epigen
 Anti-hCG antibodies -- Abgenix/AVI BioPharma
 Anti-heparanase human monoclonal antibodies -- Oxford Glycosciences/Medarex
 Anti-hepatitis C virus human monoclonal antibodies -- XTL Biopharmaceuticals
 Anti-HER-2 antibody gene therapy
 Anti-herpes antibody -- Epicyte
 Anti-HIV antibody -- Epicyte
 Anti-HIV catalytic antibody -- Hesel Biomed
 anti-HIV fusion protein -- Idun
 anti-HIV proteins -- Cangene
 Anti-HM1-24 MAb -- Chugai
 Anti-hR3 MAb
 Anti-Human-Carcinoma-Antigen MAb -- Epicyte
 Anti-ICAM-1 MAb -- Boehringer Ingelheim
 Anti-ICAM-1 MAb 1A-29 -- Pharmacia
 Anti-ICAM-1 MAb HA58
 Anti-ICAM-1 MAb YN1/1.7.4
 Anti-ICAM-3 MAb ICM3 -- ICOS
 Anti-idiotypic breast cancer vaccine 11D10
 Anti-idiotypic breast cancer vaccine ACA14C5 --
 Anti-idiotypic cancer vaccine -- ImClone Systems/Merck KGaA ImClone, Viventia Biotech
 Anti-idiotypic cancer vaccine 1A7 -- Titan
 Anti-idiotypic cancer vaccine 3H1 -- Titan
 Anti-idiotypic cancer vaccine TriAb -- Titan
 Anti-idiotypic Chlamydia trachomatis vaccine
 Anti-idiotypic colorectal cancer vaccine -- Novartis
 Anti-idiotypic colorectal cancer vaccine -- Onyvax
 Anti-idiotypic melanoma vaccine -- IDEC Pharmaceuticals
 Anti-idiotypic ovarian cancer vaccine ACA 125
 Anti-idiotypic ovarian cancer vaccine AR54 - AltaRex

FIG. 28D

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Anti-idiotypic ovarian cancer vaccine CA-125 -- AltaRex, Biomira	Anti-L-selectin monoclonal antibodies -- Protein Design Labs, Abgenix, Stanford University
Anti-IgE catalytic antibody -- Hesel Biomed	Anti-MBL monoclonal antibodies -- Alexion/Brigham and Women's Hospital
Anti-IgE MAb E26 -- Genentech	Anti-MHC monoclonal antibodies
Anti-IGF-1 MAb	Anti-MIF antibody humanised -- IDEC, Cytokine PharmaSciences
anti-inflammatory -- GeneMax	Anti-MRSA/VRSA sheep MAb -- KS Biomedix Holdings
anti-inflammatory peptide -- BTG	Anti-mu MAb -- Novartis
anti-integrin peptides -- Burnha	Anti-MUC-1 MAb
Anti-interferon-alpha-receptor MAb 64G12 -- Pharma Pacific Management	Anti-MUC 18
Anti-interferon-gamma MAb -- Protein Design Labs	Anti-Nogo-A MAb 1N1
Anti-interferon-gamma polyclonal antibody -- Advanced Biotherapy	Anti-nuclear autoantibodies -- Procyon
Anti-interleukin-10 MAb --	Anti-ovarian cancer monoclonal antibodies -- Dompe
Anti-interleukin-12 MAb --	Anti-p185 monoclonal antibodies
Anti-interleukin-1-beta polyclonal antibody -- R&D Systems	Anti-p43 MAb
Anti-interleukin-2 receptor MAb 2A3	Antiparasitic vaccines
Anti-interleukin-2 receptor MAb 33B3-1 -- Immunotech	Anti-PDGF/bFGF sheep MAb -- KS Biomedix
Anti-interleukin-2 receptor MAb ART-18	Anti-properdin monoclonal antibodies -- Abgenix/Gliatech
Anti-interleukin-2 receptor MAb LO-Tact-1	Anti-PSMA (prostate specific membrane antigen)
Anti-interleukin-2 receptor MAb Mikbeta1	Anti-PSMA MAb J591 -- BZL Biologics
Anti-interleukin-2 receptor MAb NDS61	Anti-Rev MAb gene therapy --
Anti-interleukin-4 MAb 11B11	Anti-RSV antibodies -- Epicycle, Intracell
Anti-interleukin-5 MAb -- Wallace Laboratories	Anti-RSV monoclonal antibodies -- Medarex/MedImmune, Applied Molecular Evolution/MedImmune
Anti-interleukin-6 MAb -- Centocor, Diaclone, Pharmadigm	Anti-RSV MAb, inhalation -- Alkermes/MedImmune
Anti-interleukin-8 MAb -- Abgenix	Anti-RT gene therapy
Anti-interleukin-8 MAb -- Xenotech	Antisense K-ras RNA gene therapy
Anti-JL1 MAb	Anti-SF-25 MAb
Anti-Klebsiella sheep MAb -- KS Biomedix Holdings	Anti-sperm antibody -- Epicycle
Anti-Laminin receptor MAb-liposomal doxorubicin conjugate	Anti-Tac(Fv)-PE38 conjugate
Anti-LCG MAb -- Cytoclonal	Anti-TAPA/CD81 MAb AMP1
Anti-lipopolysaccharide MAb -- VitaResc	Anti-tat gene therapy

FIG. 28E

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Anti-TCR-alphabeta MAb H57-597	AOP-RANTES -- Senetek
Anti-TCR-alphabeta MAb R73	Apan-CH -- Praecis Pharmaceuticals
Anti-tenascin MAb BC-4-I-131	APC-8024 -- Demegen
Anti-TGF-beta human monoclonal antibodies -- Cambridge Antibody Tech., Genzyme	ApoA-1 -- Milano, Pharmacia
Anti-TGF-beta MAb 2G7 -- Genentech	Apogen -- Alexion
Antithrombin III -- Genzyme Transgenics, Aventis, Bayer, Behringwerke, CSL, Myriad	apolipoprotein A1 -- Avanir
Anti-Thy1 MAb	Apolipoprotein E -- Bio-Tech. General
Anti-Thy1.1 MAb	Applaggin -- Biogen
Anti-tissue factor/factor VIIA sheep MAb -- KS Biomedix	aprotinin -- ProdiGene
Anti-TNF monoclonal antibodies -- Centocor, Chiron, Peptech, Pharmacia, Serono	APT-070C -- AdProTech
Anti-TNF sheep MAb -- KS Biomedix Holdings	AR 177 -- Aronex Pharmaceuticals
Anti-TNFalpha MAb -- Genzyme	AR 209 -- Aronex Pharmaceuticals, Antigenics
Anti-TNFalpha MAb B-C7 -- Diaclone	AR545C
Anti-tooth decay MAb -- Planet BioTech.	ARGENT gene delivery systems -- ARIAD
Anti-TRAIL receptor-1 MAb -- Takeda	Arresten
Antitumour RNases -- NIH	ART-123 -- Asahi Kasei
Anti-VCAM MAb 2A2 -- Alexion	arylsulfatase B -- BioMarin
Anti-VCAM MAb 3F4 -- Alexion	Arylsulfatase B, Recombinant human -- BioMarin
Anti-VCAM-1 MAb	AS 1051 -- Ajinomoto
Anti-VEC MAb -- ImClone	ASI-BCL -- Intracell
Anti-VEGF MAb -- Genentech	Asparaginase - Merck
Anti-VEGF MAb 2C3	ATL-101 -- Alizyme
Anti-VEGF sheep MAb -- KS Biomedix Holdings	Atrial natriuretic peptide -- Pharis
Anti-VLA-4 MAb HP1/2 -- Biogen	Aurintricarboxylic acid-high molecular weight
Anti-VLA-4 MAb PS/2	Autoimmune disorders -- GPC
Anti-VLA-4 MAb R1-2	Biotech/MorphoSys
Anti-VLA-4 MAb TA-2	Autoimmune disorders and transplant rejection -- Bristol-Myers Squibb/Genzyme
Anti-VAP-1 human MAb	Tra
Anti-VRE sheep MAb -- KS Biomedix Holdings	Autoimmune disorders/cancer -- Abgenix/Chiron, CuraGen
ANUP -- TranXenoGen	Autotaxin
ANUP-1 -- Pharis	Avicidin -- NeoRx
	axogenesis factor-1 -- Boston Life Sciences
	Axokine -- Regeneron
	B cell lymphoma vaccine -- Biomira
	B7-1 gene therapy --
	BABS proteins -- Chiron

FIG. 28F

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BAM-002 -- Novelos Therapeutics
 Basiliximab (anti CD25 MAb) -- Novartis
 Bay-16-9996 -- Bayer
 Bay-39-9437 -- Bayer
 Bay-50-4798 -- Bayer
 BB-10153 -- British Biotech
 BBT-001 -- Bolder BioTech.
 BBT-002 -- Bolder BioTech.
 BBT-003 -- Bolder BioTech.
 BBT-004 -- Bolder BioTech.
 BBT-005 -- Bolder BioTech.
 BBT-006 -- Bolder BioTech.
 BBT-007 -- Bolder BioTech.
 BCH-2763 -- Shire
 BCSF -- Millenium Biologix
 BDNF -- Regeneron -- Amgen
 Becaplermin -- Johnson & Johnson, Chiron
 Bectumomab -- Immunomedics
 Beriplast -- Aventis
 Beta-adrenergic receptor gene therapy --
 University of Arkansas
 bFGF -- Scios
 BI 51013 -- Behringwerke AG
 BIBH 1 -- Boehringer Ingelheim
 BIM-23190 -- Beaufour-Ipsen
 birch pollen immunotherapy -- Pharmacia
 bispecific fusion proteins -- NIH
 Bispecific MAb 2B1 -- Chiron
 Bitistatin
 BIWA 4 -- Boehringer Ingelheim
 blood substitute -- Northfield, Baxter Intl.
 BLP-25 -- Biomira
 BLS-0597 -- Boston Life Sciences
 BLYS -- Human Genome Sciences
 BLYS radiolabelled -- Human Genome
 Sciences
 BM 06021 -- Boehringer Mannheim
 BM-202 -- BioMarin
 BM-301 -- BioMarin
 BM-301 -- BioMarin
 BM-302 -- BioMarin
 BMP 2 -- Genetics Institute/Medtronic-
 Sofamor Danek, Genetics Institute/
 Collagenesis, Genetics
 Institute/Yamanouch
 BMP 2 gene therapy
 BMP 52 -- Aventis Pasteur, Biopharm
 BMP-2 -- Genetics Institute
 BMS 182248 -- Bristol-Myers Squibb
 BMS 202448 -- Bristol-Myers Squibb
 bone growth factors -- IsoTis
 BPC-15 -- Pfizer
 brain natriuretic peptide --
 Breast cancer -- Oxford
 GlycoSciences/Medarex
 Breast cancer vaccine -- Therion Biologics,
 Oregon
 BSSL -- PPL Therapeutics
 BST-2001 -- BioStratum
 BST-3002 -- BioStratum
 BTI 322 --
 butyrylcholinesterase -- Shire
 C 6822 -- COR Therapeutics
 C1 esterase inhibitor -- Pharming
 C3d adjuvant -- AdProTech
 CAB-2.1 -- Millennium
 calcitonin -- Inhale Therapeutics Systems,
 Aventis, Genetronics, TranXenoGen,
 Unigene, Rhone Poulenc Rohrer
 calcitonin -- oral -- Nobex, Emisphere,
 Pharmaceutical Discovery
 Calcitonin gene-related peptide -- Asahi
 Kasei -- Unigene
 calcitonin, human -- Suntory
 calcitonin, nasal -- Novartis, Unigene
 calcitonin, Panoderm -- Elan
 calcitonin, Peptitrol -- Shire
 calcitonin, salmon -- Therapicon
 calin -- Biopharm
 Calphobindin I
 calphobindin I -- Kowa
 calreticulin -- NYU

FIG. 28G

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Campath-1G
 Campath-1M
 cancer therapy -- Cangene
 cancer vaccine -- Aixlie, Aventis Pasteur,
 Center of Molecular Immunology, YM
 BioSciences, Cytos, Genzyme,
 Transgenics, GlobeImmune, Igeneon;
 ImClone, Virogenetics, InterCell, Iomai,
 Jenner Biotherapies, Memorial Sloan-
 Kettering Cancer Center, Sydney Kimmel
 Cancer Center, Novavax, Protein
 Sciences, Argonex, SIGA
 Cancer vaccine ALVAC-CEA B7.1 --
 Aventis Pasteur/Therion Biologics
 Cancer vaccine CEA-TRICOM -- Aventis
 Pasteur/Therion Biologics
 Cancer vaccine gene therapy -- Cantab
 Pharmaceuticals
 Cancer vaccine HER-2/neu -- Corixa
 Cancer vaccine THERATOPE -- Biomira
 cancer vaccine, PolyMASC -- Valentis
 Candida vaccine -- Corixa, Inhibitex
 Canstatin -- ILEX
 CAP-18 -- Panorama
 Cardiovascular gene therapy -- Collateral
 Therapeutics
 carperitide -- Suntory
 Casocidin-1 -- Pharis
 CAT 152 -- Cambridge Antibody Tech.
 CAT 192 -- Cambridge Antibody Tech.
 CAT 213 -- Cambridge Antibody Tech.
 Catalase -- Enzon
 Cat-PAD -- Circassia
 CB 0006 -- Celltech
 CCK(27-32) -- Akzo Nobel
 CCR2-641 -- NIH
 CD, Procept -- Paligent
 CD154 gene therapy
 CD39 -- Immunex
 CD39-L2 -- Hyseq
 CD39-L4 -- Hyseq
 CD4 fusion toxin -- Senetek
 CD4 IgG -- Genentech
 CD4 receptor antagonists --
 Pharmacoceia/Progenics
 CD4 soluble -- Progenics
 CD4, soluble -- Genzyme Transgenics
 CD40 ligand -- Immunex
 CD4-ricin chain A -- Genentech
 CD59 gene therapy -- Alexion
 CD8 TIL cell therapy -- Aventis Pasteur
 CD8, soluble -- Avidex
 CD95 ligand -- Roche
 CDP 571 -- Celltech
 CDP 850 -- Celltech
 CDP-860 (PEG-PDGF MAb) -- Celltech
 CDP 870 -- Celltech
 CDS-1 -- Ernest Orlando
 Cedelizumab -- Ortho-McNeil
 Cetermin -- Insmad
 CETP vaccine -- Avant
 Cetorelix
 Cetuximab
 CGH 400 -- Novartis
 CGP 42934 -- Novartis
 CGP 51901 -- Tanox
 CGRP -- Unigene
 CGS 27913 -- Novartis
 CGS 32359 -- Novartis
 Chagas disease vaccine -- Corixa
 chemokines -- Immune Response
 CHH 380 -- Novartis
 chitinase -- Genzyme, ICOS
 Chlamydia pneumoniae vaccine -- Antex
 Biologics
 Chlamydia trachomatis vaccine -- Antex
 Biologics
 Chlamydia vaccine -- GlaxoSmithKline
 Cholera vaccine CVD 103-HgR -- Swiss
 Serum and Vaccine Institute Berne
 Cholera vaccine CVD 112 -- Swiss Serum
 and Vaccine Institute Berne

FIG. 28H

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Cholera vaccine inactivated oral – SBL	CRL 1605 – CytRx
Vaccin	CS-560 – Sankyo
Chrysalin – Chrysalis BioTech.	CSF – ZymoGenetics
CI-782 – Hitachi Kase	CSF-G – Hangzhou, Dong-A, Hanmi
Ciliary neurotrophic factor – Fidia, Roche	CSF-GM – Cangene, Hunan, LG Chem
CIM project – Active Biotech	CSF-M – Zarix
CL 329753 – Wyeth-Ayerst	CT 1579 – Merck Frosst
CL22, Cobra – ML Laboratories	CT 1786 – Merck Frosst
Clenoliximab – IDEC	CT-112 ^A – BTG
Clostridium difficile antibodies – Epicyte	CTB-134L – Xenova
clotting factors – Octagene	CTC-111 – Kaketsuken
CMB 401 – Celltech	CTGF – FibroGen
CNTF – Sigma-Tau	CTLA4-Ig – Bristol-Myers Squibb
Cocaine abuse vaccine – Cantab,	CTLA4-Ig gene therapy –
ImmuLogic, Scripps	CTP-37 – AVI BioPharma
coccidiomycosis vaccine – Arizo	C-type natriuretic peptide – Suntory
collagen – Type I – Pharming	CVS 995 – Corvas Intl.
Collagen formation inhibitors – FibroGen	CX 397 – Nikko Kyodo
Collagen/hydroxyapatite/bone growth factor	CY 1747 – Epimmune
– Aventis Pasteur, Biopharm, Orquest	CY 1748 – Epimmune
collagenase – BioSpecifics	Cyanovirin-N
Colorectal cancer vaccine – Wistar Institute	Cystic fibrosis therapy – CBR/IVAX
Component B, Recombinant – Sero	CYT 351
Connective tissue growth factor inhibitors –	cytokine Traps – Regeneron
FibroGen/Taisho	cytokines – Enzon, Cytoconal
Contortrostatin	Cytomegalovirus glycoprotein vaccine –
contraceptive vaccine – Zonagen	Chiron, Aquila Biopharmaceuticals,
Contraceptive vaccine hCG	Aventis Pasteur, Virogenetics
Contraceptive vaccine male reversible –	Cytomegalovirus vaccine live – Aventis
IMMUCON	Pasteur
Contraceptive vaccine zona pellucida –	Cytosine deaminase gene therapy –
Zonagen	GlaxoSmithKline
Copper-64 labelled MAb TETA-1A3 – NCI	DA-3003 – Dong-A
Coralyn	DAB389interleukin-6 – Senetek
Corsein M	DAB389interleukin-7
C-peptide analogues – Schwarz	Daclizumab (anti-IL2R MAb) – Protein
CPI-1500 – Consensus	Design Labs
CRF – Neurobiological Tech.	DAMP ^A – Incyte Genomics
cRGDFV pentapeptide –	Daniplestim – Pharmacia
CRL 1095 – CytRx	darbepoetin alfa – Amgen
CRL 1336 – CytRx	DBI-3019 – Diabetogen

FIG. 281

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DCC -- Genzyme
 DDF -- Hyseq
 decorin -- Integra, Telios
 defensins -- Large Scale Biology
 DEGR-VIIa
 Deimmunised antibody 3B6/22 AGEN
 Deimmunised anti-cancer antibodies --
 Biovation/Viragen
 Dendroamide A
 Dengue vaccine -- Bavarian Nordic, Merck
 denileukin difitox -- Ligand
 DES-1101 -- Desmos
 desirudin -- Novartis
 desmopressin -- Unigene
 Desmoteplase -- Merck, Schering AG
 Destabilase
 Diabetes gene therapy -- DeveloGen, Pfizer
 Diabetes therapy -- Crucell
 Diabetes type 1 vaccine -- Diamyd
 Therapeutics
 DiaCIM -- YM BioSciences
 dialytic oligopeptides -- Research Corp
 Diamyd -- Diamyd Therapeutics
 DiaPep227 -- Peppen
 DiavaX -- Corixa
 Digoxin MAB -- Glaxo
 Diphtheria tetanus pertussis-hepatitis B
 vaccine -- GlaxoSmithKline
 DIR therapy -- Solis Therapeutics --
 DNase -- Genentech
 Dornase alfa -- Genentech
 Dornase alfa, inhalation -- Genentech
 Doxorubicin-anti-CEA MAb conjugate --
 Immunomedics
 DP-107 -- Trimeris
 drotrecogin alfa -- Eli Lilly
 DTctGMCSF
 DTP-polio vaccine -- Aventis Pasteur
 DU 257-KM231 antibody conjugate --
 Kyowa
 dural graft matrix -- Integra
 Duteplase -- Baxter Intl.
 DWP-401 -- Daewoong
 DWP-404 -- Daewoong
 DWP-408 -- Daewoong
 Dx 88 (Epi-KAL2) -- Dyax
 Dx 890 (elastin inhibitors) -- Dyax
 E coli O157 vaccine -- NIH
 E21-R -- BresaGen
 Eastern equine encephalitis virus vaccine --
 Echicetin --
 Echinhibin 1 --
 Echistatin -- Merck
 Echitamine --
 Ecomeximab -- Kyowa Hakko
 EC-SOD -- PPL Therapeutics
 Eculizumab (5G1.1) -- Alexion
 EDF -- Ajinomoto
 EDN derivative -- NIH
 EDNA -- NIH
 Edobacomab -- XOMA
 Edrecolomab -- Centocor
 EF 5077
 Efalizumab -- Genentech
 EGF fusion toxin -- Seragen, Ligand
 EGF-P64k vaccine -- Center of Molecular
 Immunology
 EL 246 -- LigoCyte
 elastase inhibitor -- Synergen
 elcatonin -- Therapicon
 EMD 72000 -- Merck KGaA
 Emdogain -- BIORA
 emfilmerin -- AMRAD
 Emoctakin -- Novartis
 enamel matrix protein -- BIORA
 Endo III -- NYU
 endostatin -- EntreMed, Pharis
 Enhancins -- Micrologix
 Enlimomab -- Isis Pharm.
 Enoxaparin sodium -- Pharmuka
 enzyme linked antibody nutrient depletion
 therapy -- KS Biomedix Holdings

FIG. 28J

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Eosinophil-derived neutralizing agent – EP-51216 – Asta Medica	Factor VII – Novo Nordisk, Bayer, Baxter Intl.
EP-51389 – Asta Medica	Factor VIIa – PPL Therapeutics, ZymoGenetics
EPH family ligands – Regeneron	Factor VIII – Bayer Genentech, Beaufour-Ipsen, CLB, Inex, Octagen, Pharmacia, Pharming
Epidermal growth factor – Hitachi Kasei, Johnson & Johnson	Factor VIII – PEGylated – Bayer
Epidermal growth factor fusion toxin – Senetek	Factor VIII fragments – Pharmacia
Epidermal growth factor-genistein – EP-HNE-4 – Dyax	Factor VIII gene therapy – Targeted Genetics
EPH-KAL2 – Dyax	Factor VIII sucrose formulation – Bayer, Genentech
Epoetin-alfa – Amgen, Dragon Pharmaceuticals, Nanjing Huaxin	Factor VIII-2 – Bayer
Epratuzumab – Immunomedics	Factor VIII-3 – Bayer
Epstein-Barr virus vaccine – Aviron/SmithKline Beecham, Bioresearch	Factor Xa inhibitors – Merck, Novo Nordisk, Mochida
Eptacog alfa – Novo Nordisk	Factor XII – ZymoGenetics
Eptifibatide – COR Therapeutics	Factors VIII and IX gene therapy – Genetics Institute/Targeted Genetics
erb-38 –	Famoxin – Genset
Erlizumab – Genentech	Fas (delta) TM protein – LXR BioTech.
erythropoietin – Alkermes, ProLease, Dong-A, Elanex, Genetics Institute, LG Chem, Protein Sciences, Serono, Snow Brand, SRC VB VECTOR, Transkaryotic Therapies	Fas TR – Human Genome Sciences
Erythropoietin Beta – Hoffman La Roche	Felvizumab – Scotgen
Erythropoietin/Epoetin alfa – Chugai	FFR-VIIa – Novo Nordisk
Escherichia coli vaccine – North American Vaccine, SBL Vaccin, Swiss Serum and Vaccine Institute Berne	FG-001 – F-Gene
etanercept – Immunex	FG-002 – F-Gene
examorelin – Mediolanum	FG-004 – F-Gene
Exendin 4 – Amylin	FG-005 – F-Gene
exonuclease VII	FGF + fibrin – Repair
F 105 – Centocor	Fibrimage – Bio-Tech. General
F-992 – Fornix	fibrin-binding peptides – ISIS Innovation
Factor IX – Alpha Therapeutics, Wellfide Corp., CSL, Genetics Institute/AHP, Pharmacia, PPL Therapeutics	fibrinogen – PPL Therapeutics, Pharming
Factor IX gene therapy – Cell Genesys	fibroblast growth factor – Chiron, NYU, Ramot, ZymoGenetics
	fibrolase conjugate – Schering AG
	Filgrastim – Amgen
	filgrastim – PDA modified – Xencor
	FLT-3 ligand – Immunex
	FN18 CRM9 –

FIG. 28K

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folliculin -- Biotech Australia, Human Therapeutics	glutamate decarboxylase -- Genzyme Transgenics
folliculin alfa -- Alkermes, ProLease, PowderJect, Serono, Akzo Nobel	Glycoprotein S3 -- Kureha
Folliculin Beta -- Bayer, Organon	GM-CSF -- Immunex
FP 59	GM-CSF tumour vaccine -- PowderJect
FSH -- Ferring	GnRH immunotherapeutic -- Protherics
FSH + LH -- Ferring	Goserelin (LhRH antagonist) -- AstraZeneca
F-spondin -- CeNeS	gp75 antigen -- ImClone
fusion protein delivery system -- UAB Research Foundation	gp96 -- Antigenics
fusion toxins -- Boston Life Sciences	GPI 0100 -- Galenica
G 5598 -- Genentech	GR 4991W93 -- GlaxoSmithKline
GA-II -- Transkaryotic Therapies	Granulocyte colony-stimulating factor -- Dong-A
Gamma-interferon analogues -- SRC VB VECTOR	Granulocyte colony-stimulating factor conjugate
Ganirelix -- Roche	grass allergy therapy -- Dynavax
gastric lipase -- Meristem	GRF1-44 -- ICN
Gavilimomab --	Growth Factor -- Chiron, Atrigel, Atrix, Innogenetics, ZymoGenetics, Novo
G-CSF -- Amgen, SRC VB VECTOR	growth factor peptides -- Biotherapeutics
GDF-1 -- CeNeS	growth hormone -- LG Chem
GDF-5 -- Biopharm	growth hormone, Recombinant human -- Serono
GDNF (glial derived neurotrophic factor) -- Amgen	GT 4086 -- Glatech
gelsolin -- Biogen	GW 353430 -- GlaxoSmithKline
Gemtuzumab ozogamicin -- Celltech	GW-278884 -- GlaxoSmithKline
Gene-activated epoetin-alfa -- Aventis Pharma -- Transkaryotic Therapies	H 11 -- Viventia Biotech
Glanzmann thrombasthenia gene therapy --	H5N1 influenza A virus vaccine -- Protein Sciences
Glatiramer acetate -- Yeda	haemoglobin -- Biopure
glial growth factor 2 -- CeNeS	haemoglobin 3011, Recombinant -- Baxter Healthcare
GLP-1 -- Amylin, Suntory, TheraTech, Watson	haemoglobin crosfumaril -- Baxter Intl.
GLP-1 peptide analogues -- Zealand Pharmaceuticals	haemoglobin stabilized -- Ajinomoto
glucagon -- Eli Lilly, ZymoGenetics	haemoglobin, recombinant -- Apex
Glucagon-like peptide-1 7-36 amide -- Suntory	HAF -- Immune Response
Glucocogen-like peptide -- Amylin	Hantavirus vaccine
Glucocerebrosidase -- Genzyme	HB 19
	HBNF -- Regeneron
	HCC-1 -- Pharis
	hCG -- Milkhaus

FIG. 28L

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hCG vaccine -- Zonagen
 HE-317 -- Hollis-Eden Pharmaceuticals
 Heat shock protein cancer and influenza vaccines -- StressGen
 Helicobacter pylori vaccine -- Acambis, AstraZeneca/CSL, Chiron, Provalis
 Helistat-G -- GalaGen
 Hemolink -- Hemosol
 heparinase -- Snow Brand
 heparinase -- InSight
 heparinase I -- Ibex
 heparinase III -- Ibex
 Hepatitis A vaccine -- American Biogenetic Sciences
 Hepatitis A vaccine inactivated
 Hepatitis A vaccine Nothav -- Chiron
 Hepatitis A-hepatitis B vaccine -- GlaxoSmithKline
 hepatitis B therapy -- Tripep
 Hepatitis B vaccine -- Amgen, Chiron SpA, Meiji Milk, NIS, Prodeva, PowderJect, Rhein Biotech
 Hepatitis B vaccine recombinant -- Evans Vaccines, Eptec Combiotech, Genentech, MedImmune, Merck Sharp & Dohme, Rhein Biotech, Shantha Biotechnics, Vector, Yeda
 Hepatitis B vaccine recombinant TGP 943 -- Takeda
 Hepatitis C vaccine -- Bavarian Nordic, Chiron, Innogenetics Acambis, Hepatitis D vaccine -- Chiron Vaccines
 Hepatitis E vaccine recombinant -- Genelabs/GlaxoSmithKline, Novavax
 hepatocyte growth factor -- Panorama, Sosei
 hepatocyte growth factor kringle fragments -- EntrelMed
 Her-2/Neu peptides -- Corixa
 Herpes simplex glycoprotein DNA vaccine -- Merck, Wyeth-Lederle Vaccines-Malvern, Genentech, GlaxoSmithKline, Chiron, Takeda
 Herpes simplex vaccine -- Cantab Pharmaceuticals, CEL-SCI, Henderson Morley
 Herpes simplex vaccine live -- ImClone Systems/Wyeth-Lederle, Aventis Pasteur
 HGF derivatives -- Dompe
 hIAPP vaccine -- Crucell
 Hib-hepatitis B vaccine -- Aventis Pasteur
 HIC 1
 HIP -- Altachem
 Hirudins -- Biopharma, Cangene, Dongkook, Japan Energy Corporation, Pharmacia Corporation, SIR International, Sanofi-Synthelabo, Sotragene, Rhein Biotech
 HIV edible vaccine -- ProdiGene
 HIV gp120 vaccine -- Chiron, Ajinomoto, GlaxoSmithKline, ID Vaccine, Progenics, VaxGen
 HIV gp120 vaccine gene therapy --
 HIV gp160 DNA vaccine -- PowderJect, Aventis Pasteur, Oncogen, Hyland Immuno, Protein Sciences
 HIV gp41 vaccine -- Panacos
 HIV HGP-30W vaccine -- CEL-SCI
 HIV immune globulin -- Abbott, Chiron
 HIV peptides -- American Home Products
 HIV vaccine -- Applied bioTech., Axis Genetics, Biogen, Bristol-Myers Squibb, Genentech, Korea Green Cross, NIS, Oncogen, Protein Sciences Corporation, Terumo, Tonen Corporation, Wyeth-Ayerst, Wyeth-Lederle Vaccines-Malvern, Advanced BioScience Laboratories, Bavarian Nordic, Bavarian Nordic/Statens Serum Institute, GeneCure, Immune Response, Progenics, Therion Biologics, United Biomedical, Chiron

FIG. 28M

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HIV vaccine vCP1433 -- Aventis Pasteur	Human monoclonal antibodies --
HIV vaccine vCP1452 -- Aventis Pasteur	Medarex/Northwest Biotherapeutics,
HIV vaccine vCP205 -- Aventis Pasteur	Medarex/Seattle Genetics
HL-9 -- American BioScience	human netrin-1 -- Exelixis
HM-9239 -- Cytran	human papillomavirus antibodies -- Epicyte
HML-103 -- Hemosol	Human papillomavirus vaccine -- Biotech
HML-104 -- Hemosol	Australia, IDEC, StressGen
HML-105 -- Hemosol	Human papillomavirus vaccine MEDI 501 --
HML-109 -- Hemosol	MedImmune/GlaxoSmithKline
HML-110 -- Hemosol	Human papillomavirus vaccine MEDI
HML-121 -- Hemosol	503/MEDI 504 --
hNLP -- Pharis	MedImmune/GlaxoSmithKline
Hookworm vaccine	Human papillomavirus vaccine TA-CIN --
host-vector vaccines -- Henogen	Cantab Pharmaceuticals
HPM 1 -- Chugai	Human papillomavirus vaccine TA-HPV --
HPV vaccine -- MediGene	Cantab Pharmaceuticals
HSA -- Meristem	Human papillomavirus vaccine TH-GW --
HSF -- StressGen	Cantab/GlaxoSmithKline
HSP carriers -- Weizmann, Yeda, Peptor	human polyclonal antibodies -- Biosite/Eos
HSPPC-70 -- Antigenics	BioTech./ Medarex
HSPPC-96, pathogen-derived -- Antigenics	human type II anti factor VIII monoclonal
HSV 863 -- Novartis	antibodies -- ThromboGenics
HTLV-I DNA vaccine	humanised anti glycoprotein 1b murine
HTLV-I vaccine	monoclonal antibodies -- ThromboGenics
HTLV-II vaccine -- Access	HumaRAD -- Intracell
HU 901 -- Tanox	HuMax EGFR -- Genmab
Hu23F2G -- ICOS	HuMax-CD4 -- Medarex
HuHMFG1	HuMax-IL15 -- Genmab
HumaLYM -- Intracell	HYB 190 -- Hybridon
Human krebs statika -- Yamanouchi	HYB 676 -- Hybridon
human monoclonal antibodies --	I-125 MAb A33 -- Celltech
Abgenix/Biogen, Abgenix/ Corixa,	Ibritumomab tiuxetan -- IDEC
Abgenix/ Immunex, Abgenix/Lexicon,	IBT-9401 -- Ibex
Abgenix/ Pfizer, Athersys/Medarex,	IBT-9402 -- Ibex
Biogen/MorphoSys, CAT/Searle,	IC 14 -- ICOS
Centocor/Medarex, Corixa/Kirin Brewery,	I darubicin anti-Ly-2.1 --
Corixa/Medarex, Eos BioTech./Medarex,	IDEC 114 -- IDEC
Eos/Xenex, Exelixis/Protein Design	IDEC 131 -- IDEC
Labs, ImmunoGen/ Raven, Medarex/	IDEC 152 -- IDEC
B.Twelve, MorphoSys/ImmunoGen, XTL	IDM 1 -- IDM
Biopharmaceuticals/Dyax,	IDPS -- Hollis-Eden Pharmaceuticals

FIG. 28N

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iduronate-2-sulfatase -- Transkaryotic Therapies
 IGF/IBP-2-13 -- Pharis
 IGN-101 -- Igeneon
 IK HIR02 -- Iketon
 IL-11 -- Genetics Institute/AHP
 IL-13-PE38 -- NeoPharm
 IL-17 receptor -- Immunex
 IL-18BP -- Yeda
 IL-1Hy1 -- Hyseq
 IL-1 β -- Celltech
 IL-1 β adjuvant -- Celltech
 IL-2 -- Chiron
 IL-2 + IL-12 -- Hoffman La-Roche
 IL-6/sIL-6R fusion -- Hadasit
 IL-6R derivative -- Tosoh
 IL-7-Dap 389 fusion toxin -- Ligand
 IM-862 -- Cytran
 IMC-1C11 -- ImClone
 imiglucerase -- Genzyme
 Immune globulin intravenous (human) -- Hoffman La Roche
 immune privilege factor -- Proneuron
 Immunocal -- Immunotec
 Immunogene therapy -- Briana Bio-Tech
 Immunoliposomal 5-fluorodeoxyuridine-dipalmitate --
 immunosuppressant vaccine -- Aixie
 immunotoxin -- Antisoma, NIH
 ImmuRAIT-Re-188 -- Immunomedics
 imreg-1 -- Imreg
 infertility -- Johnson & Johnson, E-TRANS
 Infliximab -- Centocor
 Influenza virus vaccine -- Aventis Pasteur, Protein Sciences
 inhibit -- Biotech Australia, Human Therapeutics
 Inhibitory G protein gene therapy
 INKP-2001 -- InKine
 Inolimomab -- Diaclone
 insulin -- Autolimmune, Altea, Biobras, BioSante, Bio-Tech. General, Chong Kun Dang, Emisphere, Flamel, Provalis, Rhein Biotech, TranXenoGen
 insulin (bovine) -- Novartis
 insulin analogue -- Eli Lilly
 Insulin Aspart -- Novo Nordisk
 insulin detemir -- Novo Nordisk
 insulin glargine -- Aventis
 insulin inhaled -- Inhale Therapeutics Systems, Alkermes
 insulin oral -- Inovax
 insulin, AeroDose -- AeroGen
 insulin, AERx -- Aradigm
 insulin, BEODAS -- Elan
 insulin, Biphasix -- Helix
 insulin, buccal -- Generex
 insulin, I2R -- Flemington
 insulin, intranasal -- Bentley
 insulin, oral -- Nobex, Unigene
 insulin, Orasome -- Endorex
 insulin, ProMaxx -- Epic
 insulin, Quadrant -- Elan
 insulin, recombinant -- Aventis
 insulin, Spiros -- Elan
 insulin, Transfersome -- IDEA
 insulin, Zymo, recombinant -- Novo Nordisk
 insulintropin -- Scios
 Insulysin gene therapy --
 integrin antagonists -- Merck
 interferon (Alpha2) -- SRC VB VECTOR, Viragen, Dong-A, Hoffman La-Roche, Genentech
 interferon -- BioMedicines, Human Genome Sciences
 interferon (Alfa-n3) -- Interferon Sciences Intl.
 interferon (Alpha), Biphasix -- Helix

FIG. 280

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interferon (Alpha)—Amgen, BioNative,
 Novartis, Genzyme Transgenics,
 Hayashibara, Inhale Therapeutics
 Systems, Medusa, Flamel, Dong-A,
 GeneTrol, Nasteck, Shantha,
 Wassermann, LG Chem, Sumitomo,
 Aventis, Behring EGIS, Pepgen, Servier,
 Rhein Biotech,
 interferon (Alpha2A)
 interferon (Alpha2B) — Enzon, Schering-
 Plough, Biogen, IDEA
 interferon (Alpha-N1) — GlaxoSmithKline
 interferon (beta) — Rentschler, GeneTrol,
 Meristem, Rhein Biotech, Toray, Yeda,
 Daiichi, Mochida
 interferon (Beta1A) — Sero, Biogen
 interferon (beta1A), inhale — Biogen
 interferon (B1b)— Chiron
 interferon (tau)— Pepgen
 Interferon alfacon-1 — Amgen
 Interferon alpha-2a vaccine
 Interferon Beta 1b — Schering/Chiron,
 InterMune
 Interferon Gamma — Boehringer Ingelheim,
 Sheffield, Rentschler, Hayashibara
 interferon receptor, Type I — Sero
 interferon(Gamma1B) — Genentech
 Interferon-alpha-2b + ribavirin — Biogen,
 ICN
 interferon-alpha-2b gene therapy —
 Schering-Plough
 Interferon-con1 gene therapy —
 interleukin-1 antagonists — Dompe
 interleukin-1 receptor antagonist — Abbott
 Bioresearch, Pharmacia
 interleukin-1 receptor type I — Immunex
 interleukin-1 receptor Type II — Immunex
 Interleukin-1 trap — Regeneron
 Interleukin-1-alpha — Immunex/Roche
 interleukin-2 — SRC VB VECTOR,
 Ajinomoto, Biomira, Chiron
 IL-2/ diphtheria toxin — Ligand
 Interleukin-3 — Cangene
 Interleukin-4 — Immunology Ventures,
 Sanofi Winthrop, Schering-Plough,
 Immunex/ Sanofi Winthrop, Bayer, Ono
 interleukin-4 + TNF-Alpha — NIH
 interleukin-4 agonist — Bayer
 interleukin-4 fusion toxin — Ligand
 Interleukin-4 receptor — Immunex, Immun
 Interleukin-6 — Ajinomoto, Cangene, Yeda,
 Genetics Institute, Novartis
 interleukin-6 fusion protein
 Interleukin-6 fusion toxin — Ligand, Sero
 interleukin-7 — IC Innovations
 interleukin-7 receptor — Immunex
 interleukin-8 antagonists — Kyowa
 Hakko/Millennium/Pfizer
 interleukin-9 antagonists — Genaera
 Interleukin-10 — DNAX, Schering-Plough
 Interleukin-10 gene therapy —
 interleukin-12 — Genetics Institute, Hoffman
 La-Roche
 interleukin-13 — Sanofi
 interleukin-13 antagonists — AMRAD
 Interleukin-13-PE38QQR
 interleukin-15 — Immunex
 interleukin-16 — Research Corp
 interleukin-18 — GlaxoSmithKline
 Interleukin-18 binding protein — Sero
 Ior-P3 — Center of Molecular Immunology
 IP-10 — NIH
 IPF — Metabolex
 IR-501 — Immune Response
 ISIS 9125 — Isis Pharmaceuticals
 ISURF No. 1554 — Millennium
 ISURF No. 1866 — Iowa State Univer.
 ITF-1697 — Italfarmaco
 Ix-162 — Ixion
 J 695 — Cambridge Antibody Tech.,
 Genetics Inst., Knoll
 Jagged + FGF — Repair

FIG. 28P

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JKC-362 -- Phoenix Pharmaceuticals
 JTP-2942 -- Japan Tobacco
 Juman monoclonal antibodies -- Medarex/Raven
 K02 -- Axys Pharmaceuticals
 Kelliximab -- IDEC
 Keyhole limpet haemocyanin
 KGF -- Amgen
 KM 871 -- Kyowa
 KPI 135 -- Scios
 KPI-022 -- Scios
 Kringle 5
 KSB 304
 KSB-201 -- KS Biomedix
 L 696418 -- Merck
 L 703801 -- Merck
 L1 -- Acorda
 L-761191 -- Merck
 lactoferrin -- Meristem, Pharming, Agennix
 lactoferrin cardio -- Pharming
 LAG-3 -- Serono
 LAIT -- GEMMA
 LAK cell cytotoxin -- Arizona
 lamellarins -- PharmaMar/University of Malaga
 laminin A peptides -- NIH
 lanotepase -- Genetics Institute
 laronidase -- BioMarin
 Lassa fever vaccine
 LCAT -- NIH
 LDP 01 -- Millennium
 LDP 02 -- Millennium
 Lecithinized superoxide dismutase -- Seikagaku
 LeIF adjuvant -- Corixa
 leishmaniasis vaccine -- Corixa
 lenercept -- Hoffman La-Roche
 Lenograstim -- Aventis, Chugai
 lepirudin -- Aventis
 leptin -- Amgen, IC Innovations
 Leptin gene therapy -- Chiron Corporation
 leptin, 2nd-generation -- Amgen
 leridistim -- Pharmacia
 leuprolide, ProMaxx -- Epic
 leuporellin, oral -- Unigene
 LeuTech -- Papatin
 LEX 032 -- SuperGen
 LIDEPT -- Novartis
 Lintuzumab (anti-CD33 MAb) -- Protein Design Labs
 lipase -- Altus Biologics
 lipid A vaccine -- EntreMed
 lipid-linked anchor Tech. -- ICRT, ID Biomedical
 liposome-CD4 Tech. -- Sheffield
 Listeria monocytogenes vaccine
 LMB 1
 LMB 7
 LMB 9 -- Battelle Memorial Institute, NIH
 LM-CD45 -- Cantab Pharmaceuticals
 lovastatin -- Merck
 LSA-3
 LT-B receptor -- Biogen
 lung cancer vaccine -- Corixa
 lusupultide -- Scios
 L-Vax -- AVAX
 LY 355455 -- Eli Lilly
 LY 366405 -- Eli Lilly
 LY-355101 -- Eli Lilly
 Lyme disease DNA vaccine -- Vical/Aventis Pasteur
 Lyme disease vaccine -- Aquila
 Biopharmaceuticals, Aventis, Pasteur, Symbicom, GlaxoSmithKline, Hyland
 Immuno, MedImmune
 Lymphocytic choriomeningitis virus vaccine
 lymphoma vaccine -- Biomira, Genitope
 LYP18
 lys plasminogen, recombinant
 Lysosomal storage disease gene therapy -- Avigen
 lysostaphin -- Nutrition 21

FIG. 28Q

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M 23 -- Gruenenthal
 M1 monoclonal antibodies -- Acorda
 Therapeutics
 MA 16N7C2 -- Corvas Intl.
 malaria vaccine -- GlaxoSmithKline,
 AdProTech, Antigenics, Apovia, Aventis
 Pasteur, Axis Genetics, Behringwerke,
 CDCP, Chiron Vaccines, Genzyme
 Transgenics, Hawaii, MedImmune, NIH,
 NYU, Oxxon, Roche/Saramane, Biotech
 Australia, Rx Tech
 Malaria vaccine CDC/NIIMALVAC-1
 malaria vaccine, multicomponent
 mammaglobin -- Corixa
 mammatatin -- Biotherapeutics
 mannan-binding lectin -- NatlImm
 mannan-MUC1 -- Psiron
 MAP 30
 Marinovir -- Phytera
 MARstem -- Maret
 MB-015 -- Mochida
 MBP -- ImmuLogic
 MCI-028 -- Mitsubishi-Tokyo
 MCIF -- Human Genome Sciences
 MDC -- Advanced BioScience -- Akzo
 Nobel, ICOS
 MDX 11 -- Medarex
 MDX 210 -- Medarex
 MDX 22 -- Medarex
 MDX 22
 MDX 240 -- Medarex
 MDX 33
 MDX 44 -- Medarex
 MDX 447 -- Medarex
 MDX H210 -- Medarex
 MDX RA -- Houston BioTech., Medarex
 ME-104 -- Pharmexa
 Measles vaccine
 Mecasermin -- Cephalon/Chiron; Chiron
 MEDI 488 -- MedImmune
 MEDI 500
 MEDI 507 -- BioTransplant
 melanin concentrating hormone --
 Neurocrine Biosciences
 melanocortins -- OMRF
 Melanoma monoclonal antibodies -- Viragen
 melanoma vaccine -- GlaxoSmithKline,
 Akzo Nobel, Avant, Aventis Pasteur,
 Bavarian Nordic, Biovector, CancerVax,
 Genzyme Molecular Oncology, Humbolt,
 ImClone Systems, Memorial, NYU, Oxxon
 Melanoma vaccine Magevac -- Therion
 memory enhancers -- Scios
 meningococcal B vaccine -- Chiron
 meningococcal vaccine -- CAMR
 Meningococcal vaccine group B conjugate -
 - North American Vaccine
 Meningococcal vaccine group B
 recombinant -- BioChem Vaccines,
 Microscience
 Meningococcal vaccine group Y conjugate -
 - North American Vaccine
 Meningococcal vaccine groups A B and C
 conjugate -- North American Vaccine
 Mepolizumab -- GlaxoSmithKline
 Metastatin -- EntreMed, Takeda
 Met-CkB7 -- Human Genome Sciences
 met-enkephalin -- TNI
 METH-1 -- Human Genome Sciences
 methioninase -- AntiCancer
 Methionine lyase gene therapy --
 AntiCancer
 Met-RANTES -- Genexa Biomedical,
 Sero
 Metreleptin
 Microtubule inhibitor MAB
 Immunogen/Abgenix
 MGDF -- Kirin
 MGTV -- Progenics
 micrin -- Endocrine
 microplasmin -- ThromboGenics
 MIF -- Genetics Institute

FIG. 28R

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migration inhibitory factor -- NIH	Mab 45-2D9 -- haematoporphyrin conjugate
Mim CD4.1 -- Xycte Therapies	Mab 4B4
mirostipen -- Human Genome Sciences	Mab 4E3-CPA conjugate -- BCM Oncologia
Mitumomab (BEC-2) -- ImClone Systems, Merck KGaA	Mab 4E3-daunorubicin conjugate
MK 852 -- Merck	Mab 50-6
MLN 1202 (Anti-CCR2 monoclonal antibody) -- Millenium Pharmaceuticals	Mab 50-61A -- Institut Pasteur
Mobenakin -- NIS	Mab 5A8 -- Biogen
molgramostim -- Genetics Institute, Novartis	Mab 791T/36-methotrexate conjugate
monoclonal antibodies -- Abgenix/Celltech, Immusol/ Medarex, Viragen/ Roslin Institute, Cambridge Antibody Tech./Elan	Mab 7c11.e8
Mab 108 --	Mab 7E11 C5-selenocystamine conjugate
Mab 10D5 --	Mab 93KA9 -- Novartis
Mab 14.18-interleukin-2 immunocytokine -- Lexigen	Mab A5B7-cisplatin conjugate -- Biodynamics Research, Pharmacia
Mab 14G2a --	Mab A5B7-I-131
Mab 15A10 --	Mab A7
Mab 170 -- Biomira	Mab A717 -- Exocell
Mab 177Lu CC49 --	Mab A7-zinostatin conjugate
Mab 17F9	Mab ABX-RB2 -- Abgenix
Mab 1D7	Mab ACA 11
Mab 1F7 -- Immune Network	Mab AFP-I-131 -- Immunomedics
Mab 1H10-doxorubicin conjugate	Mab AP1
Mab 26-2F	Mab AZ1
Mab 2A11	Mab B3-LysPE40 conjugate
Mab 2E1 -- RW Johnson	Mab B4 -- United Biomedical
Mab 2F5	Mab B43 Genistein-conjugate
Mab 31.1 -- International BioImmune Systems	Mab B43.13-Tc-99m -- Biomira
Mab 32 -- Cambridge Antibody Tech., Peptech	Mab B43-PAP conjugate
Mab 323A3 -- Centocor	Mab B4G7-gelonin conjugate
Mab 3C5	Mab BCM 43-daunorubicin conjugate -- BCM Oncologia
Mab 3F12	Mab BIS-1
Mab 3F8	Mab BMS 181170 -- Bristol-Myers Squibb
Mab 42/6	Mab BR55-2
Mab 425 -- Merck KGaA	Mab BW494
Mab 447-52D -- Merck Sharp & Dohme	Mab C 242-DM1 conjugate -- ImmunoGen
	Mab C242-PE conjugate
	Mab c30-6
	Mab CA208-cytorhodin-S conjugate -- Hoechst Japan
	Mab CC49 -- Enzo

FIG. 28S

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MAb ch14.18 --	MAb LL2-I-131 -- Immunomedics
MAb CH14.18-GM-CSF fusion protein -- Lexigen	MAb LL2-Y-90
MAB chCE7	MAB LS2D617 -- Hybritech
MAB CI-137 -- AMRAD	MAB LYM-1-gelonin conjugate
MAB cisplatin conjugate	MAB LYM-1-I-131
MAB CLB-CD19	MAB LYM-1-Y-90
MAB CLB-CD19v	MAB LYM-2 -- Peregrine
MAB CLL-1 -- Peregrine	MAB M195
MAB CLL-1-GM-CSF conjugate	MAB M195-bismuth 213 conjugate -- Protein Design Labs
MAB CLL-1-IL-2 conjugate -- Peregrine	MAB M195-gelonin conjugate
MAB CLN IgG -- doxorubicin conjugates	MAB M195-I-131
MAB conjugates -- Tanox	MAB M195-Y-90
MAB D612	MAB MA 33H1 -- Sanofi
MAB Dal B02	MAB MAD11
MAB DC101 -- ImClone	MAB MGB2
MAB EA 1 --	MAB MINT5
MAB EC708 -- Biovation	MAB MK2-23
MAB EP-5C7 -- Protein Design Labs	MAB MOC31 ETA(252-613) conjugate
MAB ERIC-1 -- ICRT	MAB MOC-31-In-111
MAB F105 gene therapy	MAB MOC-31-PE conjugate
MAB FC 2.15	MAB MR6 --
MAB G250 -- Centocor	MAB MRK-16 -- Aventis Pasteur
MAB GA6	MAB MS11G6
MAB GA733	MAB MX-DTPA BrE-3
MAB Gilomab-H -- Viventia Biotech	MAB MY9
MAB HB2-saporin conjugate	MAB Nd2 -- Tosoh
MAB HD 37 --	MAB NG-1 -- Hygeia
MAB HD37-ricin chain-A conjugate	MAB NM01 -- Nissin Food
MAB HNK20 -- Acambis	MAB OC 125
MAB huN901-DM1 conjugate -- ImmunoGen	MAB OC 125-CMA conjugate
MAB I-131 CC49 -- Corixa	MAB OKI-1 -- Ortho-McNeil
MAB ICO25	MAB OX52 -- Bioproducts for Science
MAB ICR12-CPG2 conjugate	MAB PMA5
MAB ICR-62	MAB PR1
MAB IRac-ricin A conjugate	MAB prost 30
MAB K1	MAB R-24
MAB KS1-4-methotrexate conjugate	MAB R-24 α Human GD3 -- Celltech
MAB L6 -- Bristol-Myers Squibb, Oncogen	MAB RFB4-ricin chain A conjugate
MAB LICO 16-88	MAB RFT5-ricin chain A conjugate
	MAB SC 1

FIG. 28T

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MAb SM-3 -- ICRT
 MAb SMART 1D10 -- Protein Design Labs
 MAb SMART ABL 364 -- Novartis
 MAb SN6f
 MAb SN6f-deglycosylated ricin A chain conjugate --
 MAb SN6j
 MAb SN7-ricin chain A conjugate
 MAb T101-Y-90 conjugate -- Hybritech
 MAb T-88 -- Chiron
 MAb TB94 -- Cancer ImmunoBiology
 MAb TEC 11
 MAb TES-23 -- Chugai
 MAb TM31 -- Avant
 MAb TNT-1 -- Cambridge Antibody Tech.,
 Peregrine
 MAb TNT-3
 MAb TNT-3 -- IL2 fusion protein --
 MAb TP3-At-211
 MAb TP3-PAP conjugate --
 MAb UJ13A -- ICRT
 MAb UN3
 MAb ZME-018-gelonin conjugate
 MAb-BC2 -- GlaxoSmithKline
 MAb-DM1 conjugate -- ImmunoGen
 MAb-ricin-chain-A conjugate -- XOMA
 MAb-temoporfin conjugates
 Monopharm C -- Viventia Biotech
 monteplase -- Eisai
 montirelin hydrate -- Gruenthal
 moroctocog alfa -- Genetics Institute
 Moroctocog-alfa -- Pharmacia
 MP 4
 MP-121 -- Biopharm
 MP-52 -- Biopharm
 MRA -- Chugai
 MS 28168 -- Mitsui Chemicals, Nihon
 Schering
 MSH fusion toxin -- Ligand
 MSI-99 -- Genaera
 MT 201 -- Micromet
 Muc-1 vaccine -- Corixa
 mucosal tolerance -- Aberdeen
 mullerian inhibiting subst
 muplestim -- Genetics Institute, Novartis,
 DSM Anti-Infectives
 murine MAb -- KS Biomedix
 Mutant somatropin -- JCR Pharmaceutical
 MV 833 -- Toagosei
 Mycoplasma pulmonis vaccine
 Mycoprex -- XOMA
 myeloperoxidase -- Henogen
 myostatin -- Genetics Institute
 Nacolumab tafenoxy -- Pharmacia
 Nagrecor -- Scios
 nagrestipen -- British Biotech
 NAP-5 -- Corvas Intl.
 NAPc2 -- Corvas Intl.
 nartogastim -- Kyowa
 Natalizumab -- Protein Design Labs
 Nateplase -- NIH, Nihon Schering
 nateplase -- Schering AG
 NBI-3001 -- Neurocrine Biosci.
 NBI-5788 -- Neurocrine Biosci.
 NBI-6024 -- Neurocrine Biosci.
 Nef inhibitors -- BRI
 Neisseria gonorrhoea vaccine -- Antex
 Biologics
 Neomycin B-arginine conjugate
 Nerelimomab -- Chiron
 Nerve growth factor -- Amgen -- Chiron,
 Genentech
 Nerve growth factor gene therapy
 nesiritide citrate -- Scios
 neuregulin-2 -- CeNeS
 neurocan -- NYU
 neuronal delivery system -- CAMR
 Neurophil inhibitory Factor -- Corvas
 Neuroprotective vaccine -- University of
 Auckland
 neurotrophic chimaeras -- Regeneron
 neurotrophic factor -- NsGene, CereMedix

FIG. 28U

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NeuroVax -- Immune Response
 neuritin -- Genentech
 neutral endopeptidase -- Genentech
 NGF enhancers -- NeuroSearch
 NHL vaccine -- Large Scale Biology
 NIP45 -- Boston Life Sciences
 NK1-B20
 NM 01 -- Nissin Food
 NMI-139 -- NitroMed
 NMMP -- Genetics Institute
 NN-2211 -- Novo Nordisk
 Noggin -- Regeneron
 Nonacog alfa
 Norelin -- Biostar
 Norwalk virus vaccine
 NRLU 10 -- NeoRx
 NRLU 10 PE -- NeoRx
 NT-3 -- Regeneron
 NT-4/5 -- Genentech
 NU 3056
 NU 3076
 NX 1838 -- Gilead Sciences
 NY ESO-1/CAG-3 antigen -- NIH
 NYVAC-7 -- Aventis Pasteur
 NZ-1002 -- Novazyme
 obesity therapy -- Nobex
 OC 10426 -- Ontogen
 OC 144093 -- Ontogen
 OCIF -- Sankyo
 Oct-43 -- Otsuka
 Odulimomab -- Immunotech
 OK PSA - liposomal
 OKT3-gamma-1-ala-ala
 OM 991
 OM 992
 Omalizumab -- Genentech
 oncoimmunin-L -- NIH
 Oncolysin B -- ImmunoGen
 Oncolysin CD6 -- ImmunoGen
 Oncolysin M -- ImmunoGen
 Oncolysin S -- ImmunoGen

Oncophage -- Antigenics
 Oncostatin M -- Bristol-Myers Squibb
 OncoVax-CL -- Jenner Biotherapies
 OncoVax-P -- Jenner Biotherapies
 oncept -- Yeda
 onychomycosis vaccine -- Boehringer
 Ingelheim
 opebecan -- XOMA
 opioids -- Arizona
 Oprelvekin -- Genetics Institute
 Oregovomab -- AltaRex
 Org-33408 b -- Akzo Nobel
 Orlip DP -- EpiCept
 oryzacystatin
 OSA peptides -- GenSci Regeneration
 osteoblast-cadherin GF -- Pharis
 Osteocalcin-thymidine kinase gene therapy
 osteogenic protein -- Curis
 osteopontin -- OraPharma
 osteoporosis peptides -- Integra, Telios
 osteoprotegerin -- Amgen, SnowBrand
 otitis media vaccines -- Antex Biologics
 ovarian cancer -- University of Alabama
 OX40-igG fusion protein -- Cantab, Xenova
 P 246 -- Diatide
 P 30 -- Alfacell
 p1025 -- Active Biotech
 P-113^A -- Demegen
 P-16 peptide -- Transition Therapeutics
 p43 -- Ramot
 P-50 peptide -- Transition Therapeutics
 p53 + RAS vaccine -- NIH, NCI
 PACAP(1-27) analogue
 paediatric vaccines -- Chiron
 Pafase -- ICOS
 PAGE-4 plasmid DNA -- IDEC
 PAI-2 -- Biotech Australia, Human
 Therapeutics
 Palifermin (keratinocyte growth factor) --
 Amgen
 Palivizumab -- MedImmune

FIG. 28V

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PAM 4 -- Merck	PEG-uricase -- Mountain View
paniteplase -- Yamanouchi	Pegvisomant -- Genentech
pancreatin, Minitabs -- Eurand	PEGylated proteins, PolyMASC -- Valentis
Pangen -- Fournier	PEGylated recombinant native human leptin
Pantarin -- Selective Genetics	-- Roche
Parainfluenza virus vaccine -- Pharmacia,	Pemtumomab
Pierre Fabre	Penetratin -- Cyclacel
paraoxanase -- Esperion	Pepscan -- Antisoma
parathyroid hormone -- Abiogen, Korea	peptide G -- Peptech, ICRT
Green Cross	peptide vaccine -- NIH, NCI
Parathyroid hormone (1-34) --	Pexelizumab
Chugai/Suntory	pexiganan acetate -- Genaera
Parkinson's disease gene therapy -- Cell	Pharmaprojects No. 3179 -- NYU
Genesys/ Ceregene	Pharmaprojects No. 3390 -- Ernest Orlando
Parvovirus vaccine -- MedImmune	Pharmaprojects No. 3417 -- Sumitomo
PCP-Scan -- Immunomedics	Pharmaprojects No. 3777 -- Acambis
PDGF -- Chiron	Pharmaprojects No. 4209 -- XOMA
PDGF cocktail -- Theratechnologies	Pharmaprojects No. 4349 -- Baxter Intl.
peanut allergy therapy -- Dynavax	Pharmaprojects No. 4651
PEG anti-ICAM MAb -- Boehringer	Pharmaprojects No. 4915 -- Avanir
Ingelheim	Pharmaprojects No. 5156 -- Rhizogenics
PEG asparaginase -- Enzon	Pharmaprojects No. 5200 -- Pfizer
PEG glucocerebrosidase	Pharmaprojects No. 5215 -- Origene
PEG hirudin -- Knoll	Pharmaprojects No. 5216 -- Origene
PEG interferon-alpha-2a -- Roche	Pharmaprojects No. 5218 -- Origene
PEG interferon-alpha-2b + ribavirin --	Pharmaprojects No. 5267 -- ML
Biogen, Enzon, ICN Pharmaceuticals,	Laboratories
Schering-Plough	Pharmaprojects No. 5373 -- MorphoSys
PEG MAb A5B7 --	Pharmaprojects No. 5493 -- Metabolex
Pegacaristim -- Amgen -- Kirin Brewery --	Pharmaprojects No. 5707 -- Genentech
ZymoGenetics	Pharmaprojects No. 5728 -- Autogen
Pegaldesleukin -- Research Corp	Pharmaprojects No. 5733 -- BioMarin
pegaspargase -- Enzon	Pharmaprojects No. 5757 -- NIH
pegfilgrastim -- Amgen	Pharmaprojects No. 5765 -- Gryphon
PEG-interferon Alpha -- Viragen	Pharmaprojects No. 5830 -- AntiCancer
PEG-interferon Alpha 2A -- Hoffman La-	Pharmaprojects No. 5839 -- Dyax
Roche	Pharmaprojects No. 5849 -- Johnson &
PEG-interferon Alpha 2B -- Schering-	Johnson
Plough	Pharmaprojects No. 5860 -- Mitsubishi-
PEG-r-hirudin -- Abbott	Tokyo
PEG-rHuMGDF -- Amgen	

FIG. 28W

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Pharmaprojects No. 5869 -- Oxford GlycoSciences	Plasminogen activators -- Abbott Laboratories, American Home Products,
Pharmaprojects No. 5883 -- Asahi Brewery	Boehringer Mannheim, Chiron
Pharmaprojects No. 5947 -- StressGen	Corporation, DuPont Pharmaceuticals, Eli
Pharmaprojects No. 5961 -- Theratechnologies	Lilly, Shionogi, Genentech, Genetics
Pharmaprojects No. 5962 -- NIH	Institute, GlaxoSmithKline, Hemispherx
Pharmaprojects No. 5966 -- NIH	Biopharma, Merck & Co, Novartis,
Pharmaprojects No. 5994 -- Pharming	Pharmacia Corporation, Wakamoto, Yeda
Pharmaprojects No. 5995 -- Pharming	plasminogen-related peptides -- Bio-Tech.
Pharmaprojects No. 6023 -- IMMUCON	General/MGH
Pharmaprojects No. 6063 -- Cytoclonal	platelet factor 4 -- RepliGen
Pharmaprojects No. 6073 -- SIDDCC	Platelet-derived growth factor -- Amgen --
Pharmaprojects No. 6115 -- Genzyme	ZymoGenetics
Pharmaprojects No. 6227 -- NIH	plusonemin-- Hayashibara
Pharmaprojects No. 6230 -- NIH	PMD-2850 -- Protherics
Pharmaprojects No. 6236 -- NIH	Pneumococcal vaccine -- Antex Biologics,
Pharmaprojects No. 6243 -- NIH	Aventis Pasteur
Pharmaprojects No. 6244 -- NIH	Pneumococcal vaccine intranasal --
Pharmaprojects No. 6281 -- Senetek	BioChem Vaccines/Biovector
Pharmaprojects No. 6365 -- NIH	PR1A3
Pharmaprojects No. 6368 -- NIH	PR-39
Pharmaprojects No. 6373 -- NIH	pralmorelin -- Kaken
Pharmaprojects No. 6408 -- Pan Pacific	Pretarget-Lymphoma -- NeoRx
Pharmaprojects No. 6410 -- Athersys	Priliximab -- Centocor
Pharmaprojects No. 6421 -- Oxford GlycoSciences	PRO 140 -- Progenics
Pharmaprojects No. 6522 -- Maxygen	PRO 2000 -- Procept
Pharmaprojects No. 6523 -- Pharis	PRO 367 -- Progenics
Pharmaprojects No. 6538 -- Maxygen	PRO 542 -- Progenics
Pharmaprojects No. 6554 -- APALEXO	pro-Apo A-I -- Esperion
Pharmaprojects No. 6560 -- Ardana	prolactin -- Genzyme
Pharmaprojects No. 6562 -- Bayer	Prosaptide TX14(A) -- Bio-Tech. General
Pharmaprojects No. 6569 -- Eos	prostate cancer antibodies -- Immunex,
Phenoxazine	UroCor
Phenylase -- Ibex	prostate cancer antibody therapy --
Pigment epithelium derived factor --	Genentech/UroGenesys,
plasminogen activator inhibitor-1,	Genotherapeutics
recombinant -- DuPont Pharmaceuticals	prostate cancer immunotherapeutics -- The
	PSMA Development Company
	prostate cancer vaccine -- Aventis Pasteur,
	Zonagen, Corixa, Dendreon, Jenner
	Biotherapies, Therion Biologics

FIG. 28X

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prostate-specific antigen -- Entremed	RD 62198
protein A -- Repligen	rDnase -- Genentech
protein adhesives -- Enzon	RDP-58 -- SangStat
protein C -- Baxter Intl., PPL Therapeutics, ZymoGenetics	RecepTox-Fce -- Keryx
protein C activator -- Gilead Sciences	RecepTox-GnRH -- Keryx, MTR Technologies
protein kinase R antagonists -- NIH	RecepTox-MBP -- Keryx, MTR Technologies
protirelin -- Takeda	recFSH -- Akzo Nobel, Organon
protocadherin 2 -- Caprion	REGA 3G12
Pro-urokinase -- Abbott, Bristol-Myers	Regavirumab -- Teijin
Squibb, Dainippon, Tosoh -- Welfide	relaxin -- Connetics Corp
P-selectin glycoprotein ligand-1 -- Genetics Institute	Renal cancer vaccine -- Macropharm
pseudomonas infections -- InterMune	repifermin -- Human Genome Sciences
Pseudomonas vaccine -- CytoVax	Respiratory syncytial virus PFP-2 vaccine -- Wyeth-Lederle
PSGL-Ig -- American Home Products	Respiratory syncytial virus vaccine -- GlaxoSmithKline, Pharmacia, Pierre Fabre
PSP-94 -- Procyon	Respiratory syncytial virus vaccine inactivated
PTH 1-34 -- Nobex	Respiratory syncytial virus-parainfluenza virus vaccine -- Aventis Pasteur, Pharmacia
Quilimmune-M -- Antigenics	Reteplase -- Boehringer Mannheim, Hoffman La-Roche
R 744 -- Roche	Retropep -- Retroscreen
R 101933	RFB4 (dsFv) PE38
R 125224 -- Sankyo	RFI 641 -- American Home Products
RA therapy -- Cardion	RFTS -- UAB Research Foundation
Rabies vaccine recombinant -- Aventis Pasteur, BioChem Vaccines, Kaketsuken Pharmaceuticals	RG 12986 -- Aventis Pasteur
RadioTheraCIM -- YM BioSciences	RG 83852 -- Aventis Pasteur
Ramot project No. 1315 -- Ramot	RG-1059 -- Repligen
Ramot project No. K-734A -- Ramot	rGCR -- NIH
Ramot project No. K-734B -- Ramot	rGLP-1 -- Restoragen
Ranibizumab (Anti-VEGF fragment) -- Genentech	rGRF -- Restoragen
RANK -- Immunex	rh Insulin -- Eli Lilly
ranpirase -- Alfacell	RHAMM targeting peptides -- Cangene
ranpirase-anti-CD22 Mab -- Alfacell	rHb1.1 -- Baxter Intl.
RANTES inhibitor -- Milan	rhCC10 -- Claragen
RAPID drug delivery systems -- ARIAD	rhCG -- Sero
rasburicase -- Sanofi	Rheumatoid arthritis gene therapy
rBPI-21, topical -- XOMA	
RC 529 -- Corixa	
rcFTR -- Genzyme Transgenics	

FIG. 28Y

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Rheumatoid arthritis vaccine -- Veterans Affairs Medical Center
 rhLH -- Serono
 Ribozyme gene therapy -- Genset
 Rickettsial vaccine recombinant
 RIGScan CR -- Neoprobe
 RIP-3 -- Rigel
 Rituximab -- Genentech
 RK-0202 -- RxKinetix
 RLT peptide -- Esperion
 rMNEI -- IVAX
 rmCRP -- Immtech
 RN-1001 -- Renovo
 RN-3 -- Renovo
 RNase conjugate -- Immunomedics
 RO 631908 -- Roche
 Rotavirus vaccine -- Merck
 RP 431 -- DuPont Pharmaceuticals
 RP-128 -- Resolution
 RPE65 gene therapy --
 RPR 110173 -- Aventis Pasteur
 RPR 115135 -- Aventis Pasteur
 RPR 116258A -- Aventis Pasteur
 rPSGL-Ig -- American Home Products
 r-SPC surfactant -- Byk Gulden
 RSV antibody -- Medimmune
 Ruplizumab -- Biogen
 rV-HER-2/neu -- Therion Biologics
 SA 1042 -- Sankyo
 sacrosidase -- Orphan Medical
 Sant 7
 Sargramostim -- Immunex
 saruplase -- Gruenenthal
 Satumomab -- Cytogen
 SB 1 -- COR Therapeutics
 SB 207448 -- GlaxoSmithKline
 SB 208651 -- GlaxoSmithKline
 SB 240683 -- GlaxoSmithKline
 SB 249415 -- GlaxoSmithKline
 SB 249417 -- GlaxoSmithKline
 SB 6 -- COR Therapeutics
 SB RA 31012 --
 SC 56929 -- Pharmacia
 SCA binding proteins -- Curis, Enzon
 scFv(14E1)-ETA Berlex Laboratories,
 Schering AG
 ScFv(FRP5)-ETA --
 ScFv6C6-PE40 --
 SCH 55700 -- Celltech
 Schistosomiasis vaccine -- Glaxo
 Wellcome/Medeva, Brazil
 SCPF -- Advanced Tissue Sciences
 scuPA-suPAR complex -- Hadasit
 SD-9427 -- Pharmacia
 SDF-1 -- Ono
 SDZ 215918 -- Novartis
 SDZ 280125 -- Novartis
 SDZ 89104 -- Novartis
 SDZ ABL 364 -- Novartis
 SDZ MMA 383 -- Novartis
 Secretin -- Ferring, Repligen
 serine protease inhbs -- Pharis
 sermorelin acetate -- Serono
 SERP-1 -- Viron
 sertenef -- Dainippon
 serum albumin, Recombinant human --
 Aventis Behring
 serum-derived factor -- Hadasit
 Sevirumab -- Novartis
 SGN 14 -- Seattle Genetics
 SGN 15 -- Seattle Genetics
 SGN 17/19 -- Seattle Genetics
 SGN 30 -- Seattle Genetics
 SGN-10 -- Seattle Genetics
 SGN-11 -- Seattle Genetics
 SH 306 -- DuPont Pharmaceuticals
 Shanvac-B -- Shantha
 Shigella flexneri vaccine -- Avant, Acambis,
 Novavax
 Shigella sonnei vaccine --
 sICAM-1 -- Boehringer Ingelheim
 Silteplase -- Genzyme

FIG. 28Z

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SIV vaccine -- Endocon, Institut Pasteur
 SK 896 -- Sanwa Kagaku Kenkyusho
 SK-827 -- Sanwa Kagaku Kenkyusho
 Skeletex -- CellFactors
 SKF 106160 -- GlaxoSmithKline
 S-nitroso-AR545C --
 SNTP -- Active Biotech
 somatostatin-1 -- GroPep, Mitsubishi-
 Tokyo, NIH
 somatostatin-1 carrier protein -- Insmed
 somatostatin -- Ferring
 Somatotropin/
 Human Growth Hormone -- Bio-Tech.
 General, Eli Lilly
 somatotropin -- Bio-Tech. General, Alkermes,
 ProLease, Aventis Behring, Biovector,
 Cangene, Dong-A, Eli Lilly, Emisphere,
 Enact, Genentech, Genzyme Transgenics,
 Grandis/Infimed, CSL, Infimed, MacroMed,
 Novartis, Novo Nordisk, Pharmacia
 Sero, TranXenoGen
 somatotropin derivative -- Schering AG
 somatotropin, AIR -- Eli Lilly
 Somatotropin, inhaled -- Eli Lilly/Alkermes
 somatotropin, Kabl -- Pharmacia
 somatotropin, Orasome -- Novo Nordisk
 Sonermin -- Dainippon Pharmaceutical
 SP(V5.2)C -- Supertek
 SPf66
 sphingomyelinase -- Genzyme
 SR 29001 -- Sanofi
 SR 41476 -- Sanofi
 SR-29001 -- Sanofi
 SS1(dsFV)-PE38 -- NeoPharm
 β 2 microglobulin -- Avidex
 β 2-microglobulin fusion proteins -- NIH
 β -amyloid peptides -- CeNeS
 β -defensin -- Pharis
 Staphylococcus aureus infections --
 Inhibitex/ZLB
 Staphylococcus aureus vaccine conjugate --
 Nabi
 Staphylococcus therapy -- Tripep
 Staphylokinase -- Biovation, Prothera,
 Thrombogenetics
 Streptococcal A vaccine -- M6
 Pharmaceuticals, North American Vaccine
 Streptococcal B vaccine -- Microscience
 Streptococcal B vaccine recombinant --
 Biochem Vaccines
 Streptococcus pyogenes vaccine
 STRL-33 -- NIH
 Subalin -- SRC VB VECTOR
 SUI5 -- United Biomedical
 SUI5-LHRH -- United Biomedical
 SUN-E3001 -- Suntory
 super high affinity monoclonal antibodies --
 YM BioSciences
 Superoxide dismutase -- Chiron, Enzon,
 Ube Industries, Bio-Tech, Yeda
 superoxide dismutase-2 -- OXIS
 suppressin -- UAB Research Foundation
 SY-161-P5 -- ThromboGenics
 SY-162 -- ThromboGenics
 Systemic lupus erythematosus vaccine --
 MedClone/VivoRx
 T cell receptor peptides -- Xoma
 T cell receptor peptide vaccine
 T4N5 liposomes -- AGI Dermatics
 TAC1, soluble -- ZymoGenetics
 targeted apoptosis -- Antisoma
 tasonermin -- Boehringer Ingelheim
 TASP
 TASP-V
 Tat peptide analogues -- NIH
 TBP I -- Yeda
 TBP II
 TBV25H -- NIH
 Tc 99m for cea1 -- Center of Molecular
 Immunology
 Tc 99m P 748 -- Diatide

FIG. 28AA

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Tc 99m votumumab -- Intracell	Tissue factor -- Genentech
Tc-99m rh-Annexin V -- Theseus Imaging	Tissue factor pathway inhibitor
teceleukin -- Biogen	TJN-135 -- Tsumura
tenecteplase -- Genentech	TM 27 -- Avant
Teriparatide -- Armour Pharmaceuticals,	TM 29 -- Avant
Asahi Kasei, Eli Lilly	TMC-151 -- Tanabe Seiyaku
terlipressin -- Ferring	TNF tumour necrosis factor -- Asahi Kasei
testisin -- AMRAD	TNF Alpha -- Cytime
Tetrafibricin -- Roche	TNF antibody -- Johnson & Johnson
TFPI -- EntreMed	TNF binding protein -- Amgen
tgD-IL-2 -- Takeda	TNF degradation product -- Oncotech
TGF-Alpha -- ZymoGenetics	TNF receptor -- Immunex
TGF- β -- Kolon	TNF receptor 1; soluble -- Amgen
TGF- β 2 -- Insmed	TNF Tumour necrosis factor-alpha -- Asahi
TGF- β 3 -- OSI	Kasei, Genentech, Mochida
Thalassaemia gene therapy -- Crucell	TNF-Alpha Inhibitor -- Tripep
TheraCIM-h-R3 -- Center of Molecular	TNFR:Fc gene therapy -- Targeted Genetics
Immunology, YM BioSciences	TNF-SAM2
Theradigm-HBV -- Epimmune	Tolerimab -- Innogenetics
Theradigm-HPV -- Epimmune	Toxoplasma gondii vaccine --
Theradigm-malaria -- Epimmune	GlaxoSmithKline
Theradigm-melanoma -- Epimmune	TP 9201 -- Telios
TheraFab -- Antisoma	TP10 -- Avant
ThGRF 1-29 -- Theratechnologies	TP20 -- Avant
ThGRF 1-44 -- Theratechnologies	tPA -- Centocor
Thrombin receptor activating peptide --	trafermin -- Scios
Abbott	TRAIL/Apo2L -- Immunex
thrombomodulin -- Iowa, Novocastra	TRAIL-R1 MAb -- Cambridge Antibody
Thrombopoietin -- Dragon Pharmaceuticals,	Technologies
Genentech	transferrin-binding proteins -- CAMR
thrombopoietin, Pliva -- Recepton	Transforming growth factor-beta-1 --
Thrombospondin 2 --	Genentech
thrombostatin -- Thromgen	transport protein -- Genesis
thymalfasin -- SciClone	Trastuzumab -- Genentech
thymocartin -- Gedeon Richter	TRH -- Ferring
thymosin Alpha1 -- NIH	Triabin -- Schering AG
thyroid stimulating hormone -- Genzyme	Triconal
tlCAM-1 -- Bayer	Triflavin
Tick anticoagulant peptide -- Merck	troponin I -- Boston Life Sciences
TIF -- Xoma	TRP-2 ^A -- NIH
Tifacogin -- Chiron, NIS, Pharmacia	trypsin inhibitor -- Mochida

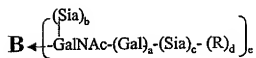
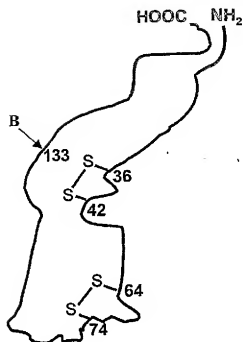
FIG. 28BB

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TSP-1 gene therapy --	Vascular endothelial growth factors -- R&D
TT-232	Systems
TTS-CD2 -- Active Biotech	vascular targeting agents -- Peregrine
Tuberculosis vaccine -- Aventis Pasteur, Genesis	vasopermeation enhancement agents -- Peregrine
Tumor Targeted Superantigens -- Active Biotech -- Pharmacia	vasostatin -- NIH
tumour vaccines -- PhotoCure	VCL -- Bio-Tech. General
tumour-activated prodrug antibody conjugates -- Millennium/ImmunoGen	VEGF -- Genentech, Scios
tumstatin -- ILEX	VEGF inhibitor -- Chugai
Tuvirumab -- Novartis	VEGF-2 -- Human Genome Sciences
TV-4710 -- Teva	VEGF-Trap -- Regeneron
TWEAK receptor -- Immunex	viscumin, recombinant -- Madaus
TXU-PAP	Vitaxin
TY-10721 -- TOA Eiyō	Vitrax -- ISTA Pharmaceuticals
Type I diabetes vaccine -- Research Corp	West Nile virus vaccine -- Bavarian Nordic
Typhoid vaccine CVD 908	WP 652
U 143677 -- Pharmacia	WT1 vaccine -- Corixa
U 81749 -- Pharmacia	WX-293 -- Wilex BioTech.
UA 1248 -- Arizona	WX-360 -- Wilex BioTech.
UGIF -- Sheffield	WX-UK1 -- Wilex BioTech.
UIC 2	XMP-500 -- XOMA
UK 101	XomaZyme-791 -- XOMA
UK-279276 -- Corvas Intl.	XTL 001 -- XTL Biopharmaceuticals
urodilatin -- Pharis	XTL 002 -- XTL Biopharmaceuticals
urofolitrophin -- Sero	yeast delivery system -- GlobImmune
Urokinase -- Abbott	Yersinia pestis vaccine
uteroferin -- Pepgen	YIGSR-Stealth -- Johnson & Johnson
V 20 -- GLYCODesign	Yissum Project No. D-0460 -- Yissum
V2 vasopressin receptor gene therapy vaccines -- Active Biotech	YM 207 -- Yamanouchi
Varicella zoster glycoprotein vaccine -- Research Corporation Technologies	YM 337 -- Protein Design Labs
Varicella zoster virus vaccine livé -- Cantab Pharmaceuticals	Yttrium-90 labelled biotin
Vascular endothelial growth factor -- Genentech, University of California	Yttrium-90-labeled anti-CEA MAb T84.66 -- ZD 0490 -- AstraZeneca
	ziconotide -- Elian
	ZK 157138 -- Berlex Laboratories
	Zollmombab aritox
	Zorcell -- Immune Response
	ZRXL peptides -- Novartis

FIG. 28CC

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a-c, c (independently selected) = 0 or 1;

d = 0;

R = modifying group, sialyl or oligosialyl

FIG. 29A

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CHO, BHK, 293 cells, Vero expressed G-CSF
a-c, e (independently selected) = 0 or 1; d = 0

- ↓
1. Sialidase
2. CMP-SA-PEG, ST3Gal1

a-d, e (independently selected) = 0 or 1;
R = PEG.

FIG. 29B

Insect cell expressed G-CSF
a, e (independently selected) = 0 or 1;
b, c, d = 0.

- ↓
1. Galactosyltransferase, UDP-Gal
2. CMP-SA-PEG, ST3Gal1

a, c, d, e (independently selected) = 0 or 1; R =
PEG.

FIG. 29C

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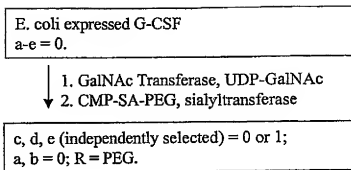


FIG. 29D

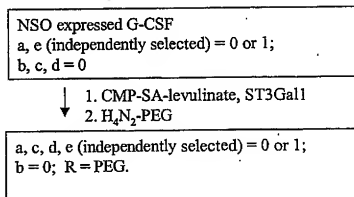


FIG. 29E

63/497

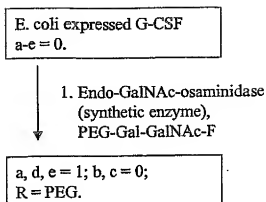


FIG. 29F

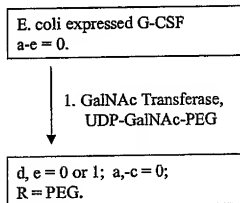
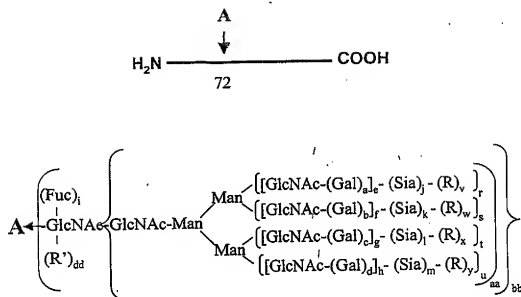


FIG. 29G

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a-d, i, n-u (independently selected) = 0 or 1.

aa, bb, cc, dd, ee (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 30A

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CHO, BHK, 293 cells, Vero expressed
interferon alpha 14C.
a-d, aa, bb = 1; e-h = 1 to 4;
cc, j-m, i, r-u (independently selected) = 0 or 1;
q, n-p, v-z, cc, dd, ee = 0.

1. Sialidase
2. CMP-SA-PEG, ST3Gal3

a-d, aa, bb = 1; e-h = 1 to 4;
bb, cc, i, r-u (independently selected) = 0 or 1;
q, n-p, v-z, cc, dd, ee = 0;
v-y (independently selected) = 1,
when j-m (independently selected) = 1;
R = PEG.

FIG. 30B

Insect cell or fungi expressed interferon alpha-14C.
a-d, f, h, j-q, s, u, v-z, cc, dd, ee = 0;
e, g, i, r, t (independently selected) = 0 or 1;
aa, bb = 1.

1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal-PEG

b, d, f, h, j-q, s, u, w, y, z, cc, dd, ee = 0;
a, c, e, g, i, r, t, v, x (independently selected) = 0 or 1;
v, x (independently selected) = 1,
when a, c, (independently selected) = 1;
aa, bb = 1; R = PEG.

FIG. 30C

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Yeast expressed interferon alpha-14C.

a-q, cc, dd, ee, v-z = 0;

r-y (independently selected) = 0 to 1;

aa, bb = 1;

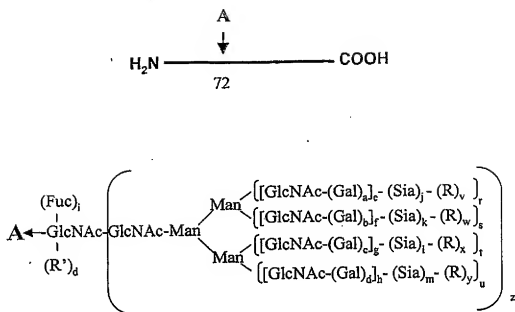
R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-PEG, ST3Gal3

a-z, bb = 0; aa = 1; R' = -Gal-Sia-PEG.

FIG. 30D

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1.

R = polymer; R' = sugar, glycoconjugate.

FIG. 30E

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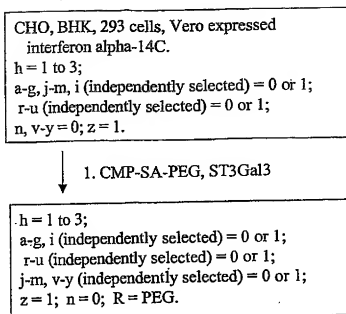


FIG. 30F

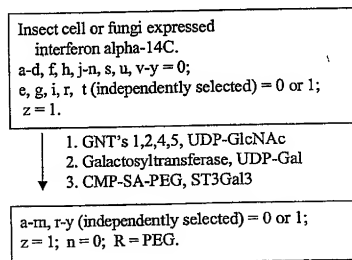


FIG. 30G

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Yeast expressed interferon alpha-14C.
 a-n = 0; r-y (independently selected) = 0 to 1;
 z = 1; R (branched or linear) = Man,
 oligomannose.

1. mannosidases
2. GNT's 1,2,4,5, UDP-GlcNAc
3. Galactosyltransferase, UDP-Gal
4. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;
 z = 1; n = 0; R = PEG.

FIG. 30H

NSO expressed interferon alpha 14C.
 a-i, r-u (independently selected) = 0 or 1;
 j-m, n, v-y = 0; z = 1.

1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
2. H₄N₂-PEG

a-i, j-m, r-y (independently selected) = 0 or 1;
 n = 0; z = 1; R = PEG.

FIG. 30I

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CHO, BHK, 293 cells, Vero expressed
interferon alpha-14C.
h = 1 to 3;
a-g, j-m, i (independently selected) = 0 or 1;
r-u (independently selected) = 0 or 1;
n, v-y = 0; z = 1.

↓
1. CMP-SA-PEG, α 2,8-ST

h = 1 to 3;
a-g, i, r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0 to 2;
v-y (independently selected) = 1,
when j-m (independently selected) is 2;
z = 1; n = 0; R = PEG.

FIG. 30J

CHO, BHK, 293 cells, Vero expressed
Interferon alpha-14C.
a-g, j-m, r-u (independently selected) = 0 or 1;
h = 1 to 3; n, v-y = 0; z = 1.

↓
1. Sialidase
2. Trans-sialidase, PEG-Sia-lactose

a-g, j-m, r-y (independently selected) = 0 or 1;
h = 1 to 3; n = 0; z = 1; R = PEG.

FIG. 30K

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CHO, BHK, 293 cells, Vero expressed
interferon alpha-14C.
h = 1 to 3;
a-g, j-m, i (independently selected) = 0 or 1;
r-u (independently selected) = 0 or 1;
n, v-y = 0; z = 1.

1. CMP-SA, α 2,8-ST

h = 1 to 3;
a-g, i, r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0 to 40;
z = 1; v-y, n = 0.

FIG. 30L

Insect cell or fungi expressed interferon alpha-14C.
a-d, f, h, j-n, s, u, v-y = 0;
e, g, i, r, t (independently selected) = 0 or 1;
z = 1.

1. GNT's 1 & 2, UDP-GlcNAc
2. Galactosyltransferase,
UDP-Gal-linker-SA-CMP
3. ST3Gal3, transferrin

a, c, e, g, i, r, t, v, x (independently selected) = 0 or 1;
z = 1; b, d, f, h, j-n, s, u, w, y = 0;
R = transferrin.

FIG. 30M

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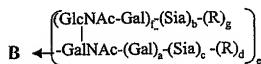
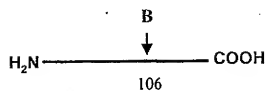
Insect cell or fungi expressed interferon alpha-14C.
a-d, f, h, j-n, s, u, v-y = 0;
e, g, i, r, t (independently selected) = 0 or 1; z = 1.

- ↓
1. endoglycanase
 2. Galactosyltransferase,
UDP-Gal-linker-SA-CMP
 3. ST3Gal3, transferrin

i (independently selected) = 0 or 1;
a-h, j-m, r-z = 0;
n = 1; R' = -Gal-linker-transferrin.

FIG. 30N

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a-c, e, f (independently selected) = 0 or 1;
d, g = 0; R = polymer, glycoconjugate.

FIG. 300

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CHO, BHK, 293 cells, Vero expressed
IF-alpha (2a or 2b).
a-c (independently selected) = 0 or 1;
e = 1; d, f, g = 0



1. Sialidase
2. CMP-SA-PEG, ST3Gal1

a-d (independently selected) = 0 or 1;
e = 1; b, f, g = 0; R = PEG.

FIG. 30P

Insect cell expressed interferon alpha (2a or 2b).
a, e (independently selected) = 0 or 1;
b, c, d, f, g = 0.



1. Galactosyltransferase, UDP-Gal
2. CMP-SA-PEG, ST3Gal1

a, c, d, e (independently selected) = 0 or 1;
b, f, g = 0; R = PEG.

FIG. 30Q

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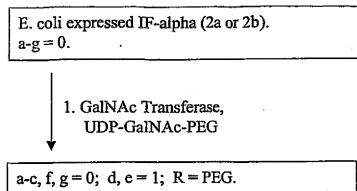


FIG. 30R

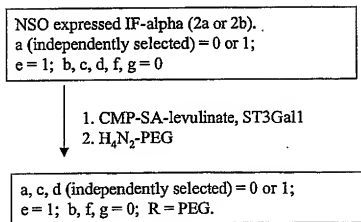


FIG. 30S

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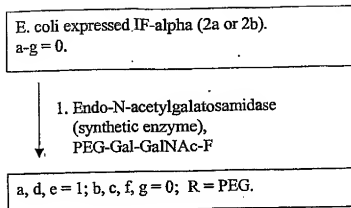


FIG. 30T

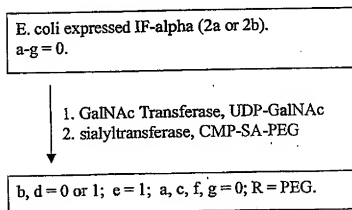


FIG. 30U

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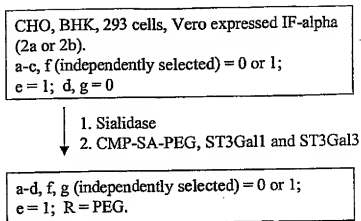


FIG. 30V

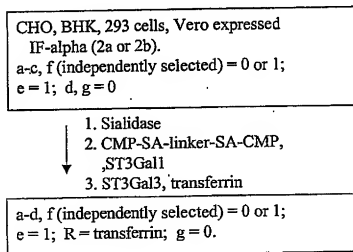
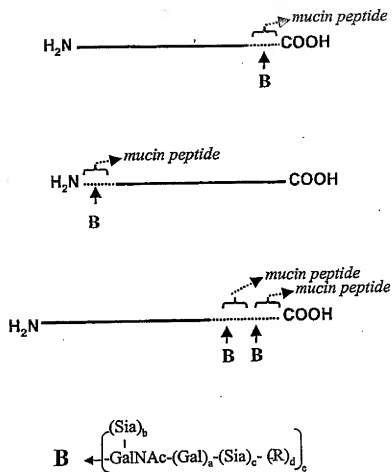


FIG. 30W

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a-c, e (independently selected) = 0 or 1;
 d = 0; R = polymer, glycoconjugate.

FIG. 30X

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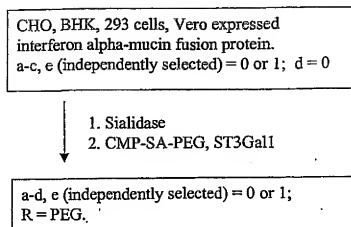


FIG. 30Y

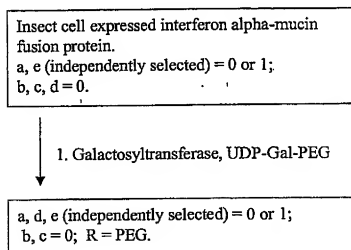


FIG. 30Z

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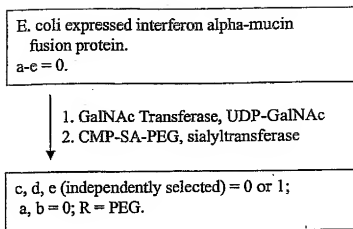
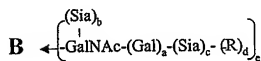
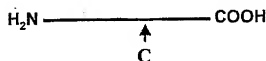
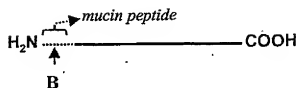


FIG. 30AA

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a-c, e (independently selected) = 0 or 1;
d = 0; R = polymer, linker.

FIG. 30BB

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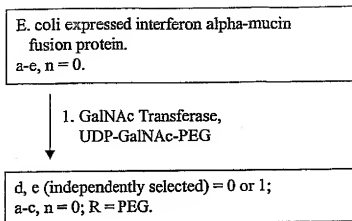


FIG. 30CC

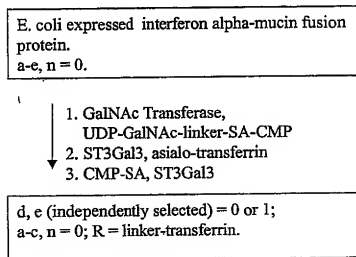


FIG. 30DD

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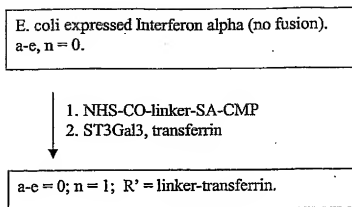
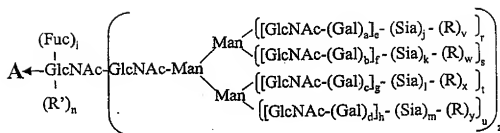


FIG. 30EE

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer

FIG. 31A

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CHO, BHK, 293 cells, Vero expressed IF-beta
 h = 1 to 3;
 a-g, j-m, i (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 n, v-y = 0; z = 1.

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3

h = 1 to 3;
 a-g, i (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 j-m, v-y (independently selected) = 0 or 1;
 z = 1; n = 0; R = PEG.

FIG. 31B

Insect cell expressed IF-beta
 a-d, f, h, j-n, s, u, v-y = 0;
 e, g, i, r, t (independently selected) = 0 or 1;
 z = 1.

- ↓
1. GNT's 1&2, UDP-GlcNAc
 2. Galactosyltransferase, UDP-Gal
 2. CMP-SA-PEG, ST3Gal3,
buffer, salt

b, d, f, h, k, m, n, s, u, w, y = 0;
 a, c, e, g, i, r, t (independently selected) = 0 or 1;
 j, l, v, x (independently selected) = 0 or 1;
 z = 1; R = PEG.

FIG. 31C

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Yeast expressed IF-beta

a-n = 0; z = 1;

r-y (independently selected) = 0 to 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-PEG, ST3Gal3

a-m, r-z = 0; n = 1; R' = -Gal-Sia-PEG.

FIG. 31D

CHO, BHK, 293 cells, Vero expressed IF-beta

h = 1 to 3;

a-g, j-m, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

n, v-y = 0; z = 1.

- ↓
1. CMP-SA-PEG, ST3Gal3

h = 1 to 3;

a-g, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

j-m, v-y (independently selected) = 0 or 1;

z = 1; n = 0; R = PEG.

FIG. 31E

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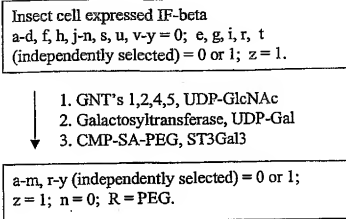


FIG. 31F

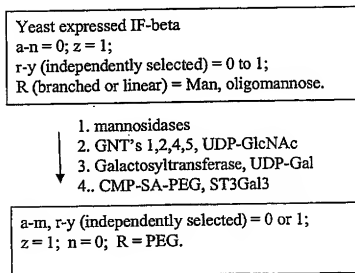


FIG. 31G

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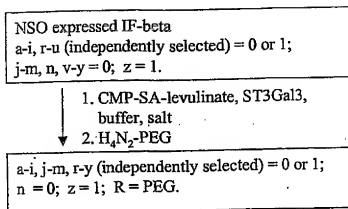


FIG. 31H

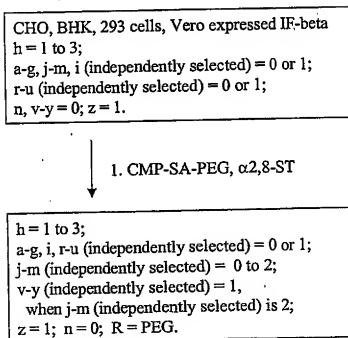


FIG. 31I

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CHO, BHK, 293 cells, Vero expressed IF-beta
a-g, j-m, r-u (independently selected) = 0 or 1;
h = 1 to 3; n, v-y = 0; z = 1.

- ↓
1. Sialidase
 2. Trans-sialidase, PEG-Sia-lactose

a-g, j-m, r-y (independently selected) = 0 or 1;
h = 1 to 3; n = 0; z = 1; R = PEG.

FIG. 31J

CHO, BHK, 293 cells, Vero expressed Ifn-beta.
a-d, i-m, r-u, z (independently selected) = 0 or 1;
e-h = 1; n, v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;
e-h = 1; n=0;
v-y (independently selected) = 0 or 1; R = PEG.

FIG. 31K

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NSO expressed Ifn-beta.

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. α -Galactosyltransferase, UDP-Gal
 - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; R = PEG

n = 0; v-y (independently selected) = 1,
when j-m (independently selected) is 1;

FIG. 31L

CHO, BHK, 293 cells, Vero expressed Ifn-beta.

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n = 0;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 31M

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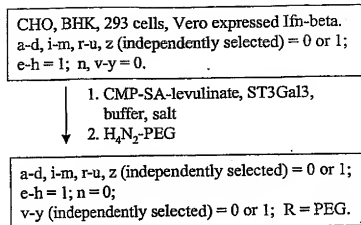


FIG. 31N

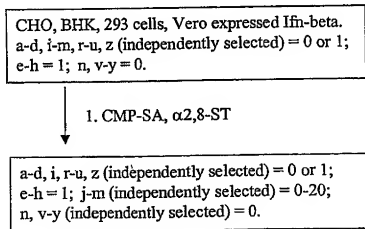
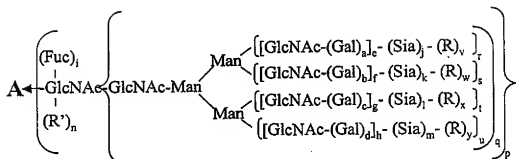
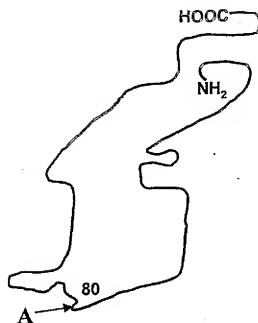


FIG. 31O

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a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group;

R' = H, glycosyl group, modifying group,
glycoconjugate.

FIG. 31P

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Insect cell expressed Ifn-beta.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 31Q

Yeast expressed Ifn-beta.

a-m = 0; q-y (independently selected) = 0 to 1;

p = 1;

R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0;

n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 31R

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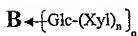
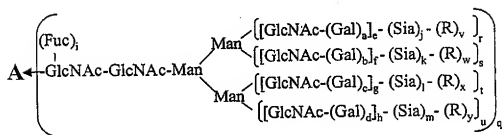
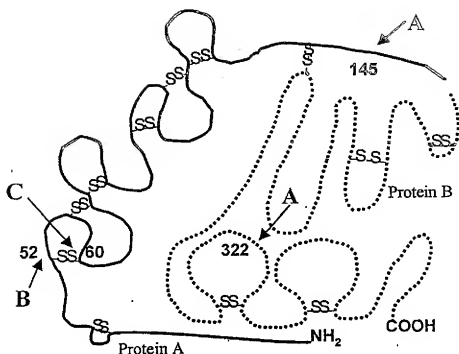
CHO, BHK, 293 cells, Vero expressed Ifn-beta.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,
ST3Gal3
 2. ST3Gal3, desialylated transferrin.
 3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 31S

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a-d, i, q-u (independently selected) = 0 or 1.

o, p (independently selected) = 0 or 1.

e-h, n (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-y = 0;

R = modifying group, mannose, oligo-mannose, Sia-Lewis X, Sia-Lewis A..

FIG. 32A

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BHK expressed Factor VII or VIIa

a-d, e, i, g, q, j, l, o, p (independently selected) = 0 or 1;
 r, t = 1; f, h, k, m, s, u, v-y = 0; n = 0-4.

1. Sialidase

2. CMP-SA-PEG (16 mole eq),
 ST3Gal3

a-d, e, g, i, q, j, l, o, p (independently selected) = 0 or 1;
 r, t = 1; f, h, k, m, s, u, w, y = 0; n = 0-4;
 v, x, (independently selected) = 1,
 when j, l (respectively, independently selected) is 1;
 R = PEG.

FIG. 32B

CHO, BHK, 293 cells, Vero expressed Factor VII or VIIa

a-d, e, i, g, q, j, l, o, p (independently selected) = 0 or 1;
 r, t = 1; f, h, k, m, s, u, v-y = 0; n = 0-4.

1. Sialidase

2. CMP-SA-PEG (1.2 mole eq),
 ST3Gal3

3. CMP-SA (8 mol eq), ST3Gal3

a-d, e, g, i, q, j, l, o, p (independently selected) = 0 or 1;
 r, t = 1; f, h, k, m, s, u, w, y = 0; n = 0-4;
 v or x, (independently selected) = 1,
 when j or l, (respectively, independently selected) is 1;
 R = PEG.

FIG. 32C

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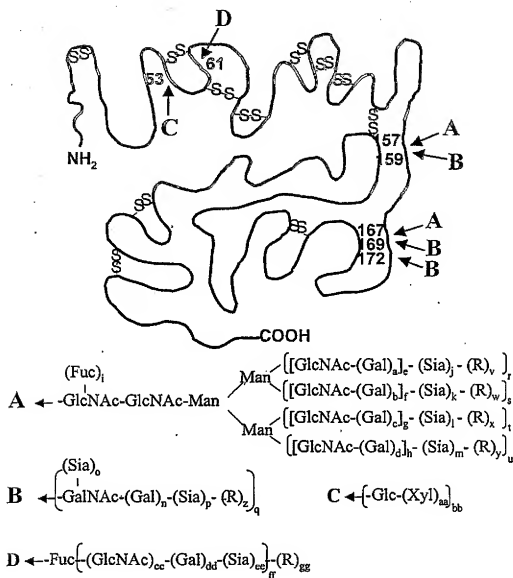
NSO expressed Factor VII or VIIa
a-u (independently selected) = 0 or 1;
v-y = 0; n = 0-4;
Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
2. Galactosyltransferase, UDP-Gal
▼ 3. CMP-SA-PEG, ST3Gal3

a-m, o-u (independently selected) = 0 or 1;
n = 0-4; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
Sia = Sia; R = PEG.

FIG. 32D

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a-d, i, n-u (independently selected) = 0 or 1.

bb, cc, dd, ee, ff, gg (independently selected) = 0 or 1.

c-h, aa (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

FIG. 33A

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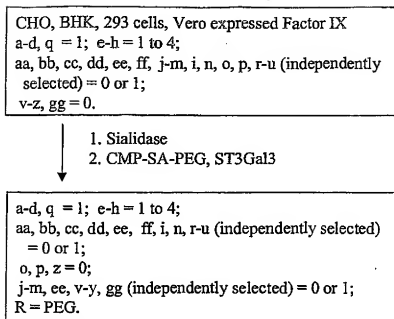


FIG. 33B

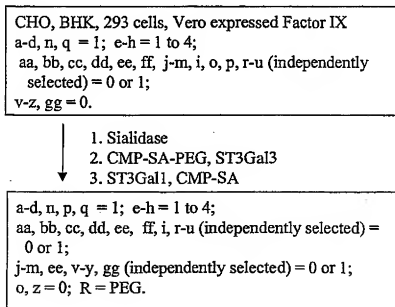


FIG. 33C

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CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q, bb, cc, dd, ff = 1; e-h, aa = 1 to 4; ee, j-m, i,
 o, p, r-u (independently selected) = 0 or 1; v-z, gg = 0.

1. sialidase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA, ST3Gal3
4. CMP-SA-PEG, ST3Gal1

a-d, n, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, r-u (independently selected) =
 0 or 1; R = PEG;
 o, v-y, gg = 0;
 j-m, p, ee (independently selected) = 0 or 1, but when
 p = 1, z = 1.

FIG. 33D

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1; R = PEG;
 o, p, z = 0; j-m, ee, v-y, gg (independently selected) =
 0 or 1.

FIG. 33E

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CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0; R = PEG;
 j-m, ee, v-y, gg (independently selected) = 0 or 1.

FIG. 33F

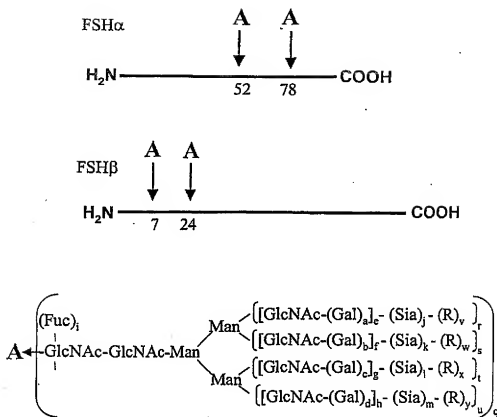
CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q, bb, cc, dd, ff = 1;
 e-h, aa = 1 to 4;
 ee, j-m, i, o, p, r-u (independently selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. CMP-SA-PEG, α2,8-ST

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0; R = PEG;
 j-m, ee (independently selected) = 0 to 2;
 v-y, gg (independently selected) = 1, when j-m
 (independently selected) is 2;

FIG. 33G

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 34A

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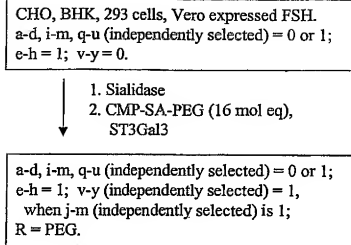


FIG. 34B

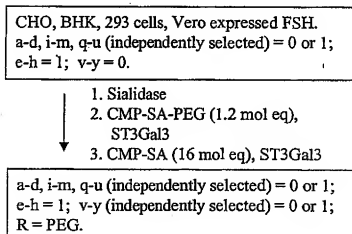


FIG. 34C

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NSO expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3
- ↓

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 34D

CHO, BHK, 293 cells, Vero expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3
- ↓

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 34E

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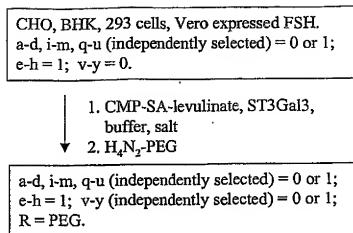


FIG. 34F

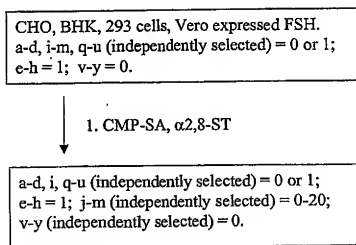


FIG. 34G

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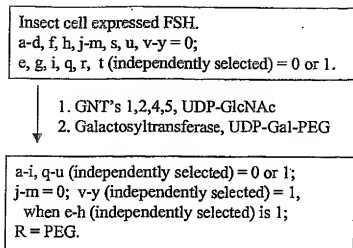


FIG. 34H

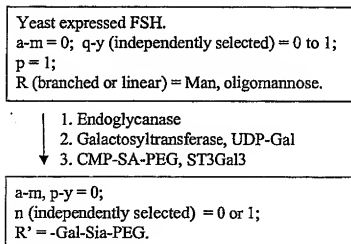


FIG. 34I

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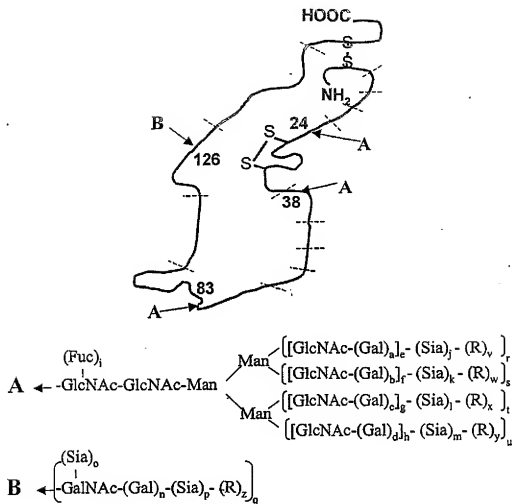
CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated chorionic gonadotrophin (CG) produced in CHO.
 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-CG.

FIG. 34J

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = polymer.

FIG. 35A

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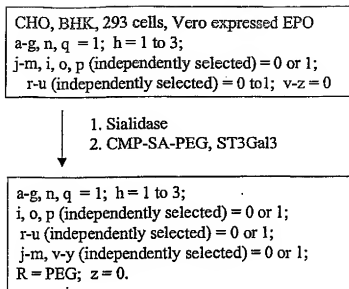


FIG. 35B

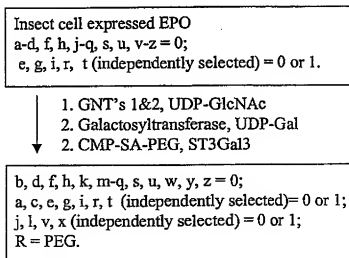


FIG. 35C

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CHO, BHK, 293 cells, Vero expressed EPO
a-q, r-u (independently selected) = 0 or 1;
v-z = 0.

1. sialidase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA, ST3Gal3
4. CMP-SA-PEG, ST3Gal1

a-h, n, q = 1;
i-m, o, r-u (independently selected) = 0 or 1;
v-y = 0; p, z = 0 or 1; R = PEG.

FIG. 35D

CHO, BHK, 293 cells, Vero expressed EPO
a-g, n, q = 1; h = 1 to 3;
j-m, i, o, p (independently selected) = 0 or 1;
r-u (independently selected) = 0 or 1;
v-z = 0

1. CMP-SA-PEG, ST3Gal3

a-g, n, q = 1; h = 1 to 3;
i, o, p (independently selected) = 0 or 1;
r-u (independently selected) = 0 to 1;
j-m, v-y (independently selected) = 0 or 1;
R = PEG; z = 0.

FIG. 35E

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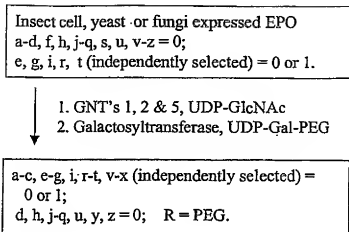


FIG. 35F

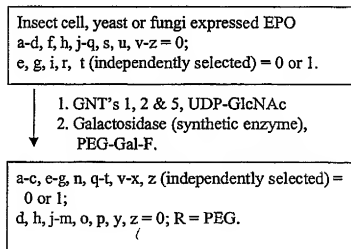


FIG. 35G

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Insect cell, yeast or fungi expressed EPO
a-d, f, h, j-m, n-q, s, u, v-z = 0;
e, g, i, r, t (independently selected) = 0 or 1.



1. GNT-1, UDP-GlcNAc-PEG

e, i, r, v (independently selected) = 0 or 1;
a-h, j-q, s-u, w-z = 0; R = PEG.

FIG. 35H

Insect cell, yeast or fungi expressed EPO
a-d, f, h, j-m, n-q, s, u, v-z = 0;
e, g, i, r, t (independently selected) = 0 or 1.



1. GNT-1, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal-PEG

a, e, i, r, v (independently selected) = 0 or 1;
b-d, f-h, j-q, s-u, w-z = 0; R = PEG.

FIG. 35I

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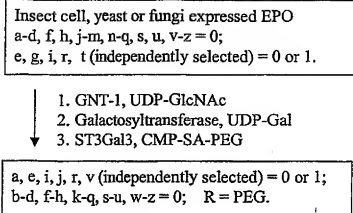


FIG. 35J

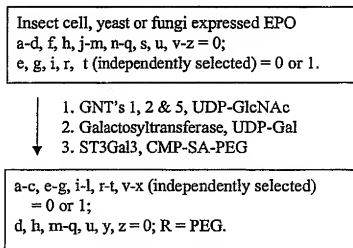


FIG. 35K

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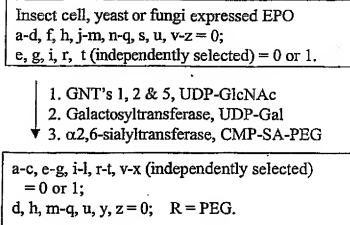


FIG. 35L

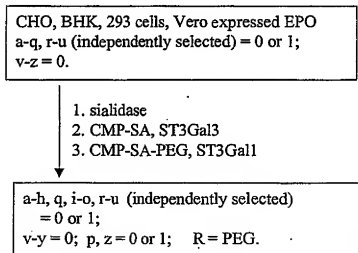


FIG. 35M

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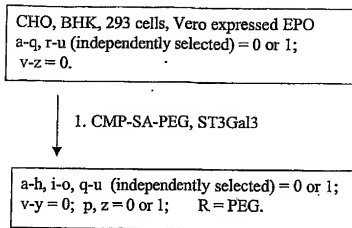


FIG. 35N

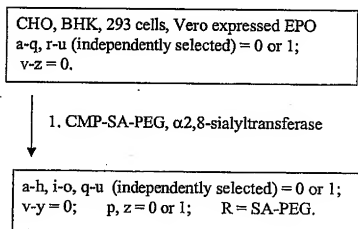


FIG. 35O

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CHO, BHK, 293 cells, Vero expressed EPO
 a-q, r-u (independently selected) = 0 or 1;
 v-z = 0.



1. CMP-SA-PEG, $\alpha 2,8$ -sialyltransferase

a-h, i-o, p-u, v-z (independently selected)
 = 0 or 1;
 R = SA-PEG.

FIG. 35P

yeast or fungi expressed EPO
 r, t, u, v, x, y (independently selected) = 0 or 1;
 a-m, n-q, s, w, z = 0; R = (Man)_n
 where n = 1-5, linear or branched.



1. mannosidases
 2. GNT-1, UDP-GlcNAc
 3. galactosyltransferase, UDP-Gal
 4. ST3Gal3, CMP-SA-PEG

a, e, j, r, v (independently selected) = 0 or 1;
 b-d, f-i, k-q, s-u, w-z = 0; R = PEG.

FIG. 35Q

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yeast or fungi expressed EPO
 r, t, u, v, x, y (independently selected) = 0 or 1;
 $a-m, n-q, s, w, z = 0$; $R = (\text{Man})_n$
 where $n = 1-5$, linear or branched.

- ↓
 1. mannosidases
 2. GNT-1, UDP-GlcNAc-PEG

e, r, v (independently selected) = 0 or 1;
 $a-h, i-q, s-u, w-z = 0$; $R = \text{PEG}$.

FIG. 35R

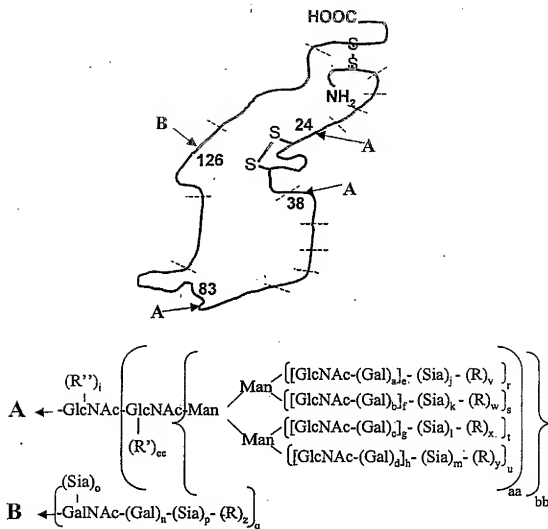
yeast or fungi expressed EPO
 r, t, u, v, x, y (independently selected) = 0 or 1;
 $a-m, n-q, s, w, z = 0$; $R = (\text{Man})_n$
 where $n = 1-5$, linear or branched.

- ↓
 1. mannosidase-I
 2. GNT-1, UDP-GlcNAc
 3. galactosyltransferase, UDP-Gal
 4. ST3Gal3, CMP-SA-PEG

$a, e, j, r, t-u, v, x, y$ (independently selected)
 = 0 or 1;
 $b-d, f-i, k-q, s, w, z = 0$;
 $(R)_v = \text{PEG}$; $(R)_x$ and $(R)_y = \text{Man}$.

FIG. 35S

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0; aa, bb = 1; cc = 0;

R = polymer; R'' and R' = sugar-polymer or Fuc.

FIG. 35T

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yeast or fungi expressed EPO
 r, t, u, v, x, y (independently selected) = 0 or 1;
 $cc, a-m, n-q, s, w, z = 0$;
 $aa, bb = 1$;
 $R = (Man)_n$, where $n = 1-100$, linear or branched.

- ↓
 1. endo-H
 ↓
 2. galactosyltransferase, UDP-Gal-PEG

i (independently selected) = 0 or 1;
 $aa, bb, cc, a-h, j-z = 0$; $R'' = \text{Gal-PEG}$.

FIG. 35U

yeast or fungi expressed EPO
 r, t, u, v, x, y (independently selected) = 0 or 1;
 $cc, a-m, n-q, s, w, z = 0$; $aa, bb = 1$;
 $R = (Man)_n$, where $n = 1-100$, linear or branched.

- ↓
 1. endo-H
 ↓
 2. galactosyltransferase, UDP-Gal
 ↓
 3. ST3Gal3, CMP-SA-PEG

i (independently selected) = 0 or 1;
 $aa, bb, cc, a-h, j-z = 0$; $R'' = \text{Gal-SA-PEG}$.

FIG. 35V

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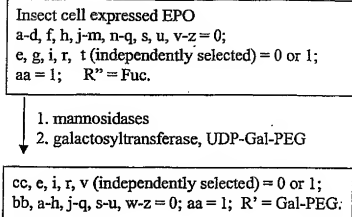
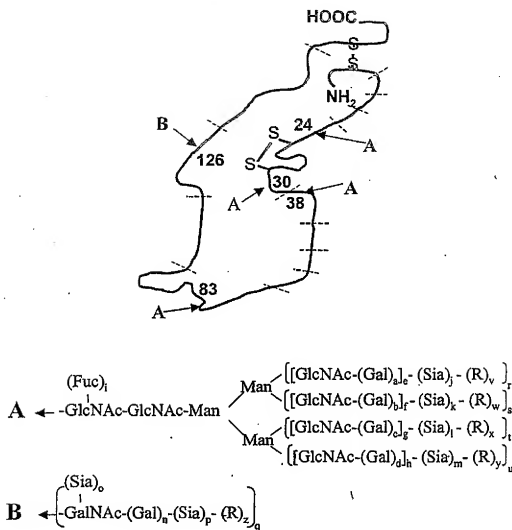


FIG. 35W

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = polymer.

FIG. 35X

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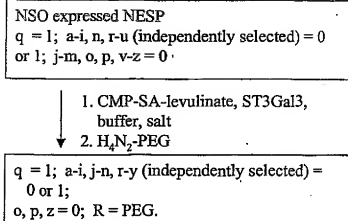


FIG. 35Y

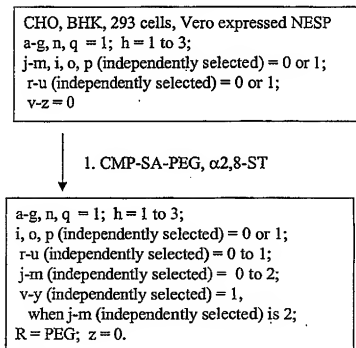


FIG. 35Z

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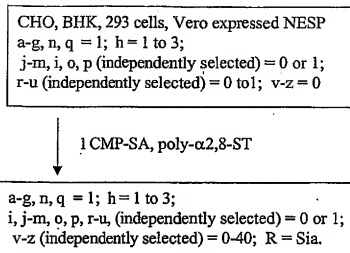
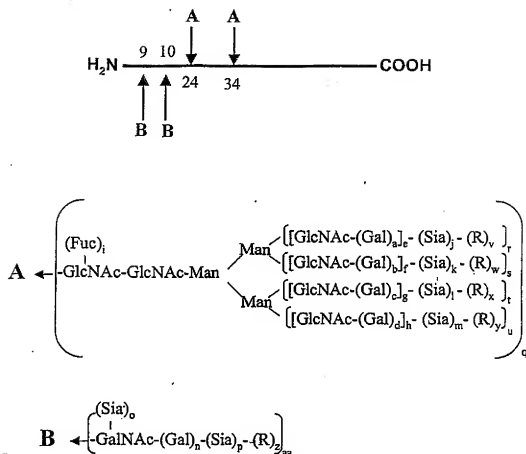


FIG. 35AA

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a-d, i, n-u, aa (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 100.
 v-y = 0; R = polymer, glycoconjugate.

FIG. 36A

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CHO, BHK, 293 cells, Vero expressed GM-CSF.
 a-d, i-m, o-u, aa (independently selected) = 0 or 1;
 n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;
 o, p, z = 0; n, e-h = 1;
 v-y (independently selected) = 1,
 when j-m (independently selected) is 1;
 R = PEG.

FIG. 36B

CHO, BHK, 293 cells, Vero expressed GM-CSF.
 a-d, i-m, o-u, aa (independently selected) = 0 or 1;
 n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3 &
ST3Gal1

a-d, i-m, p-u, aa (independently selected) = 0 or 1;
 o, z = 0; n, e-h = 1;
 v-y (independently selected) = 0 or 1; R = PEG.

FIG. 36C

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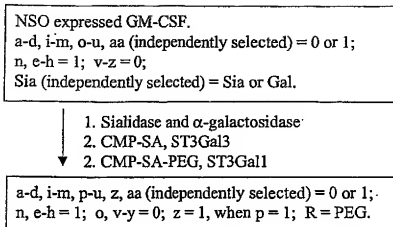


FIG. 36D

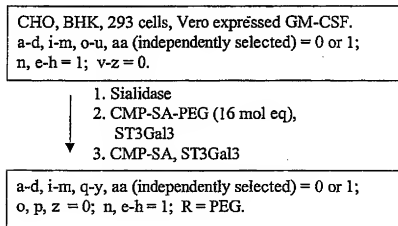


FIG. 36E

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CHO, BHK, 293 cells, Vero expressed GM-CSF.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.



1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
2. H₄N₂-PEG

a-d, i-m, o-y, aa (independently selected) = 0 or 1;
z = 0; n, e-h = 1; R = PEG.

FIG. 36F

CHO, BHK, 293 cells, Vero expressed GMCSF.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

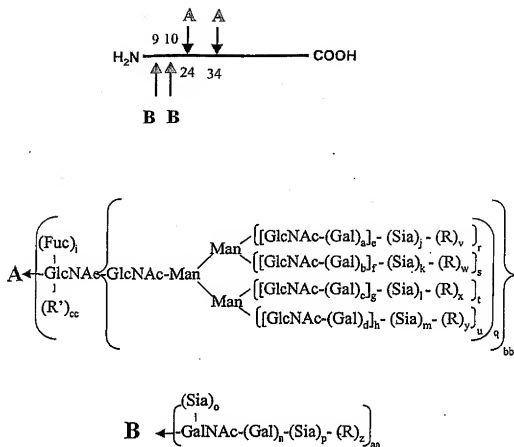


1. CMP-SA, α 2,8-ST

a-d, i, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; j-m (independently selected) = 0-20;
v-z (independently selected) = 0.

FIG. 36G

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a-d, i, n-u, aa, bb, cc (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 36H

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Insect cell expressed GM-CSF.

a-d, f, h, j-m, o, p, s, u, v-z = 0;

e, g, i, n, q, r, t, aa (independently selected) = 0 or 1.

- ↓
1. GNT's 1,2,4,5, UDP-GlcNAc
 2. Galactosyltransferase, UDP-Gal-PEG

a-i, n, q-u (independently selected) = 0 or 1;

j-m = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 36I

Yeast expressed GM-CSF.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1;

bb = 1; R (branched or linear) = Man, oligomannose;

GalNAc = Man.

- ↓
1. Endoglycanase
 2. mannosidase (if aa = 1).
 3. Galactosyltransferase, UDP-Gal-PEG

a-p, r-z, aa, bb = 0;

q, cc (independently selected) = 0 or 1;

R' = -Gal-PEG.

FIG. 36J

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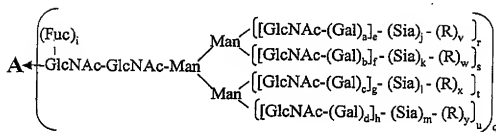
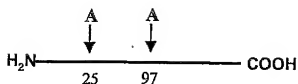
CHO, BHK, 293 cells, Vero expressed GM-CSF.
a--m, o-u, aa, bb (independently selected) = 0 or 1;
n, v-z, cc = 0.

- ↓
1. sialidase
 2. CMP-SA, ST3Gal3
 2. CMP-SA-linker-SA-CMP, ST3Gal1
 3. ST3Gal3, transferrin

a--m, p-u, z, aa (independently selected) = 0 or 1;
o, v-y, cc = 0; bb, n = 1; R = transferrin.

FIG. 36K

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 37A

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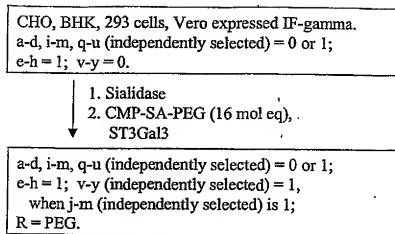


FIG. 37B

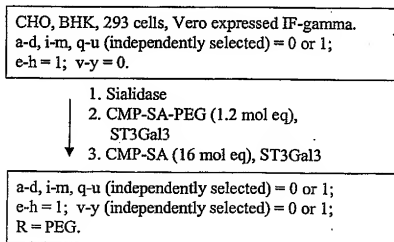


FIG. 37C

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NSO expressed Interferon gamma.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

1. Sialidase and α -galactosidase
2. α -Galactosyltransferase, UDP-Gal
- ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 37D

CHO, BHK, 293 cells, Vero expressed
Interferon gamma.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

1. Sialidase
2. CMP-SA-PEG (16 mol eq),
ST3Gal3
- ▼ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 37E

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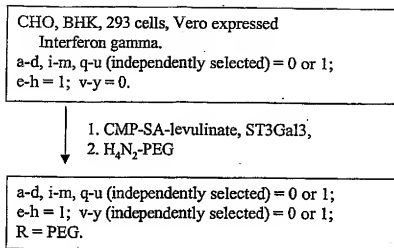


FIG. 37F

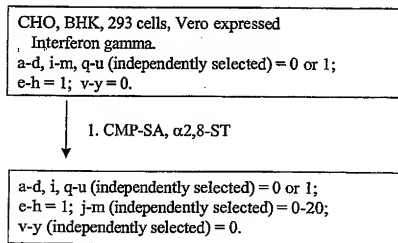


FIG. 37G

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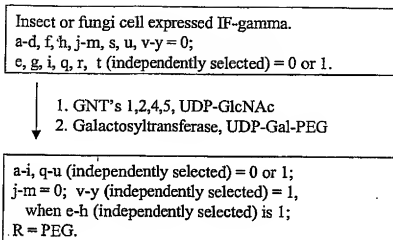


FIG. 37I

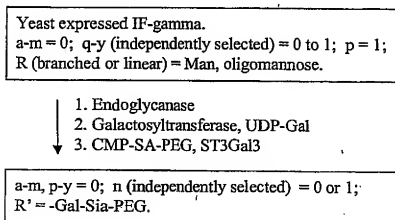


FIG. 37J

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CHO, BHK, 293 cells, Vero expressed IF-gamma.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP, ST3Gal3
 2. Galactosyltransferase, transferrin treated with endoglycanase.

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 37K

CHO, BHK, 293 cells, Vero expressed
Interferon gamma.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h, p = 1; n, v-y = 0.

- ↓
1. CMP-SA-PEG,
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h, p = 1;
n, v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 37L

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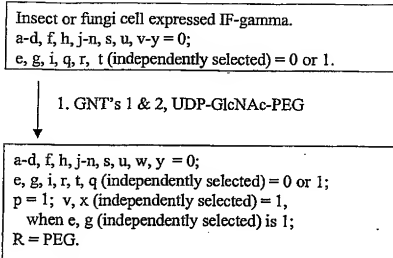


FIG. 37M

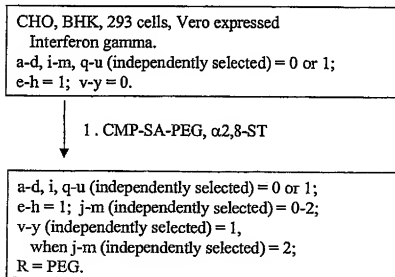


FIG. 37N

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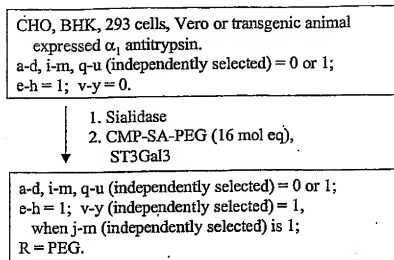


FIG. 38B

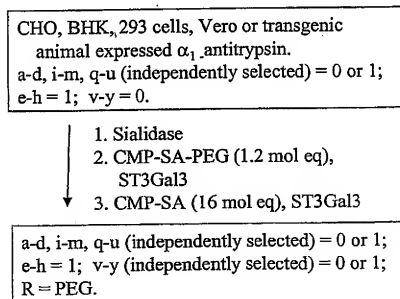


FIG. 38C

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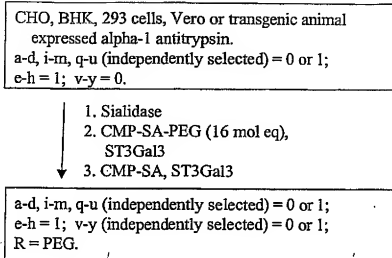


FIG. 38D

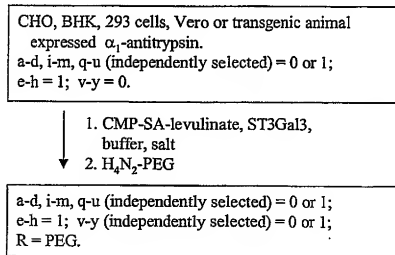


FIG. 38E

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CHO, BHK, 293 cells, Vero expressed α_1 -antitrypsin.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

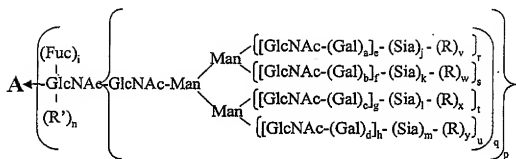
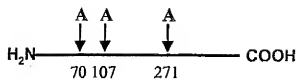


1. CMP-SA, α_2 ,8-ST

a-d, i, q-u (independently selected) = 0 or 1; e-h = 1;
j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 38F

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 38G

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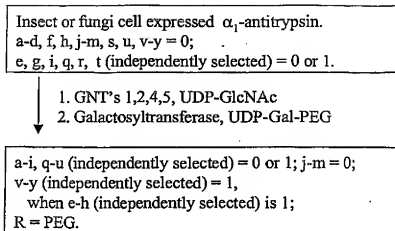


FIG. 38H

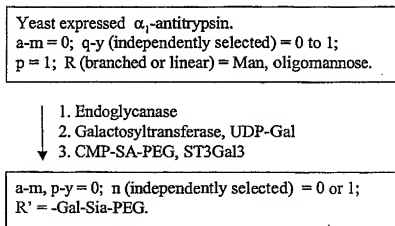


FIG. 38I

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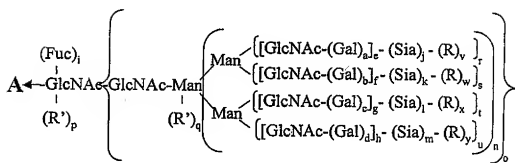
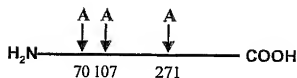
CHO, BHK, 293 cells, Vero expressed α_1 -antitrypsin.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, transferrin treated
with endoglycanase

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 38J

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer;

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 38K

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Yeast expressed alpha-1 antitrypsin.

a-h, i-m, p, q = 0;

R (independently selected) = mannose, oligomannose, polymannose;

r-u, v-y (independently selected) = 0 or 1; n, o = 1.

- ↓ 1. endoglycanase
 ↓ 2. Galactosyltransferase, UDP-Gal-PEG

a-h, i-o, q, r-u, v-y = 0; p = 1.

R' = Gal-PEG.

FIG. 38L

Plant expressed alpha-1 antitrypsin.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1;

n=1; R' = xylose

- ↓ 1. hexosaminidase,
 ↓ 2. alpha mannosidase and xylosidase
 ↓ 3. GlcNAc transferase, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, r, t (independently selected) = 0;

q = 1; R' = GlcNAc-PEG.

FIG. 38M

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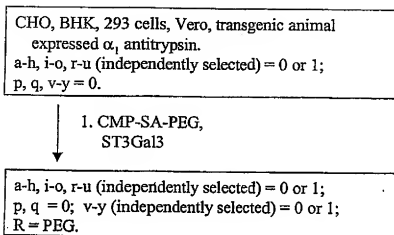
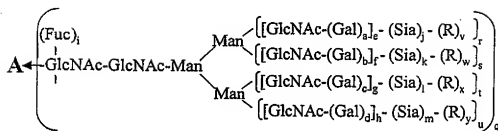
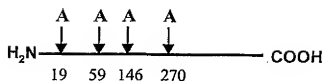


FIG. 38N

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 39A

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CHO, BHK, 293 cells, Vero expressed Cerezyme
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 39B

CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-M-6-P (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = mannose-6-phosphate

FIG. 39C

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CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = Mannose-6-phosphate

FIG. 39D

CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H_4N_2 -spacer-M-6-P or clustered M-6-P

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = M-6-P or clustered M-6-P

FIG. 39E

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CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

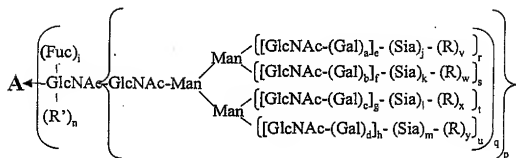
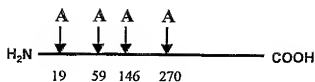


1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 39F

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 39G

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Insect cell expressed Cerezyme.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 39H

Yeast-expressed Cerezyme.

a-m = 0; q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 39I

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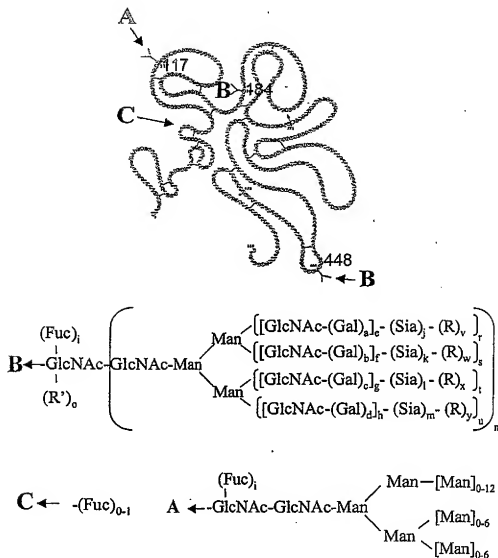
CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,
ST3Gal3
 2. ST3Gal3, desialylated transferrin.
 3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0; v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 39J

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer; R' = sugar, glycoconjugate.

FIG. 40A

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CHO, BHK, 293 cells, Vero expressed tPA
 a-g, n = 1; h = 1 to 3;
 j-m, i, (independently selected) = 0 or 1;
 r-u (independently selected) = 0 to 1; o, v-y = 0.

1. Mannosidase(s), sialidase
2. GNT1,2 (4 and/or 5) UDP-GlcNAc
3. Gal transferase, UDP-Gal
4. CMP-SA-PEG, ST3Gal3

A = B; a-g, n = 1; h = 1 to 3;
 i, r-u (independently selected) = 0 or 1;
 o = 0; j-m, v-y (independently selected) = 0 or 1;
 R = PEG

FIG. 40B

Insect or fungi cell expressed tPA
 A = B; a-d, f, h, j-o, s, u, v-y = 0;
 e, g, i, n, r, t (independently selected) = 0 or 1.

1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3

A = B; b, d, f, h, k, m, o, s, u, w, y = 0;
 a, c, e, g, i, r, t (independently selected) = 0 or 1;
 n = 1; j, l, v, x (independently selected) = 0 or 1;
 R = PEG.

FIG. 40C

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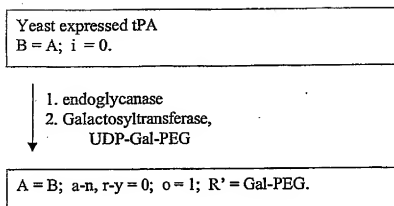


FIG. 40D

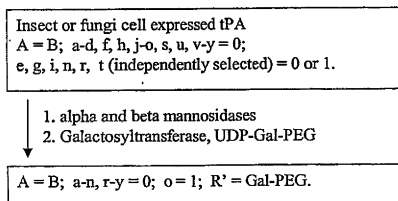


FIG. 40E

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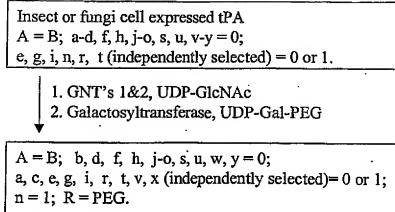


FIG. 40F

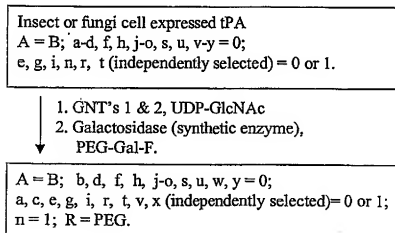
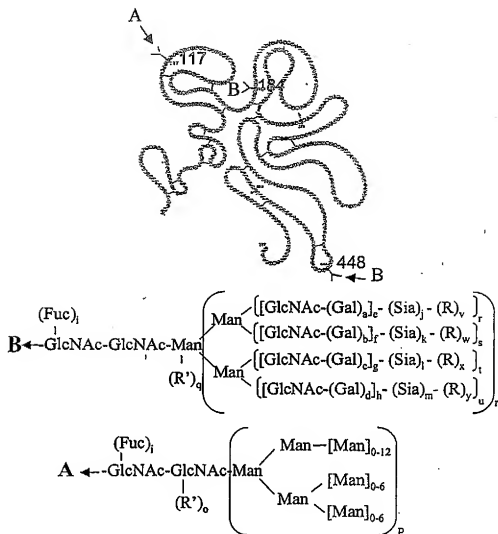


FIG. 40G

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer; R' = sugar, glycoconjugate.

FIG. 40H

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NSO expressed tPA

A = B; a-m, r-u (independently selected) = 0 or 1;
n = 1; o, p, q, v-y = 0

- ↓
1. sialidase, alpha-galactosidase
 2. CMP-SA-levulinate, ST3Gal3,
 3. H₄N₂-PEG

A = B; a-m, r-y (independently selected) = 0 or 1;
n = 1; o, p, q = 0;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 40I

CHO, BHK, 293 cells, Vero expressed tPA

a-g, n, p = 1; h = 1 to 3;
j-m, i, (independently selected) = 0 or 1;
r-u (independently selected) = 0 to 1; q, o, v-y = 0.

- ↓
1. alpha and beta Mannosidases
 2. CMP-SA, ST3Gal3
 3. Galactosyltransferase, UDP-Gal-PEG


a-g, n = 1; h = 1 to 3;
i, r-u (independently selected) = 0 or 1; o = 1;
q, p, v-y = 0; j-m (independently selected) = 0 or 1;
R' = Gal-PEG

FIG. 40J

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Plant expressed tPA

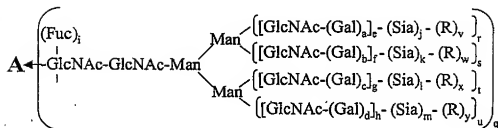
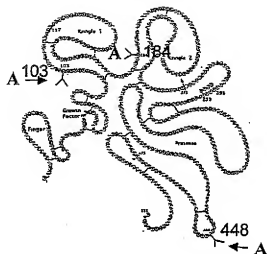
A = B; a-d, f, h, j- m, s, u, v-y = 0;
e, g, i, q, r, t (independently selected) = 0 or 1;
n = 1; R' = xylose

- 
1. hexosaminidase,
 2. alpha mannosidase and
xylosidase
 3. GlcNAc transferase, UDP-
GlcNAc-PEG

A = B; a-d, f, h, j-n, s, u, v-y = 0;
e, g, i, r, t (independently selected) = 0;
q = 1; R' = GlcNAc-PEG.

FIG. 40K

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a-d, i, q-u (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 100.
 v-y = 0; R = polymer.

FIG. 40L

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CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 40M

CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 40N

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NSO expressed TNK tPA

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

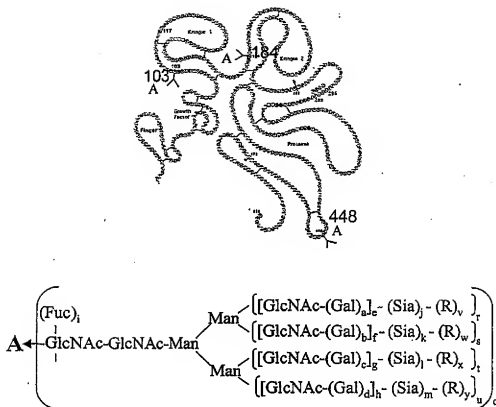
e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 400

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 40P

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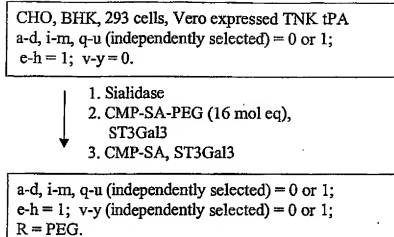


FIG. 40Q

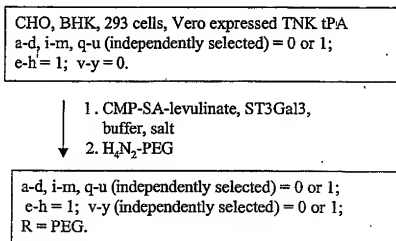


FIG. 40R

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CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

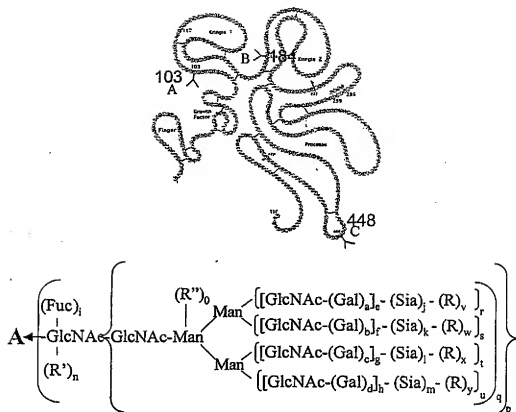


1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 40S

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a-d, i, n-y (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

R'' = glycosyl residue.

FIG. 40T

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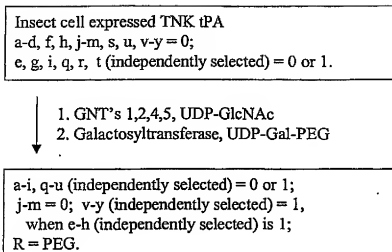


FIG. 40U

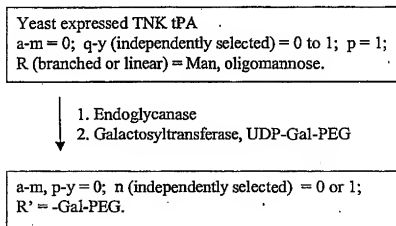


FIG. 40V

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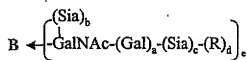
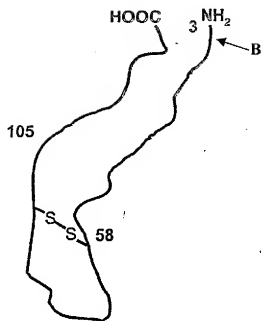
CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, anti-TNF
IG chimera produced in CHO.

a-m, r-u (independently selected) = 0 or 1; p, q = 1;
n = 0; v-y (independently selected) = 0 or 1;
R = linker-anti-TNF IG chimera protein.

FIG. 40W

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a-c, e (independently selected) = 0 or 1;
 d = 0;
 R = modifying group, mannose, oligo-
 mannose.

FIG. 41A

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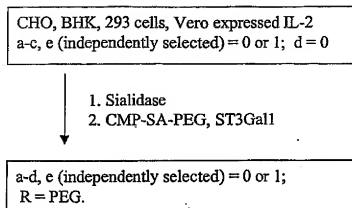


FIG. 41B

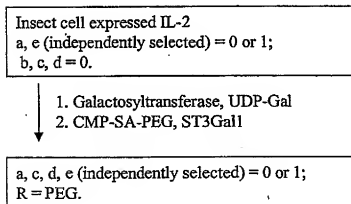


FIG. 41C

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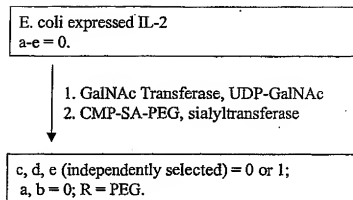


FIG. 41D

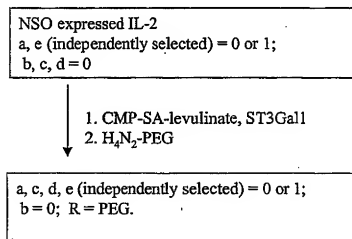


FIG. 41E

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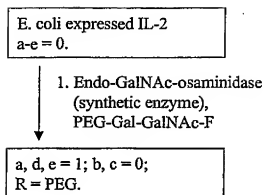


FIG. 41F

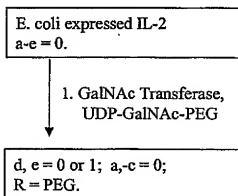
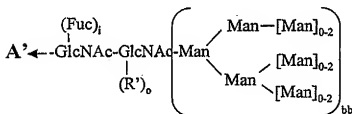
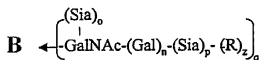
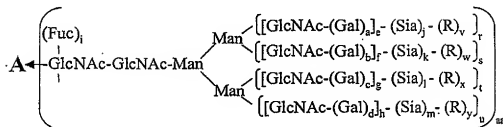


FIG. 41G

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2 peptides
A and A' - N-linked sites
B - O-linked sites



Alternate structure
for some N-linked
structures of A.

a-d, i, n-u (independently selected) = 0 or 1.
aa, bb (independently selected) = 0 or 1.
e-h (independently selected) = 0 to 6.
j-m (independently selected) = 0 to 20.
v-z = 0; R = polymer, glycoconjugate.

FIG. 42A

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CHO, BHK, 293s cells, Vero, MDCK, HEKC expressed
Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.



1. Sialidase

2. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;

aa, bb, a-d, i, n, q-u (independently selected) = 0 or 1;

o, p, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42B

CHO, BHK, 293S cells, Vero, MDCK, 293S, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.



1. Sialidase

2. CMP-SA-PEG, ST3Gal3

3. ST3Gal1, CMP-SA

e-h = 1 to 4;

aa, bb, a-d, i, n, p-u (independently selected) = 0 or 1;

o, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42C

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CHO, BHK, 293s cells, Vero, MDCK, HEKC
expressed Factor VIII.
e-h = 1 to 4;
aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;
v-z = 0.



1. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;
aa, bb, a-d, i, n-u (independently selected) = 0 or 1;
z = 0; j-m, v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 42D

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.
e-h = 1 to 4;
aa, bb, a-d, j-m, i, n-u (independently selected) 0 or 1;
v-z = 0.



1. CMP-SA-PEG, ST3Gal1

e-h = 1 to 4;
aa, bb, a-d, i, n-u (independently selected) = 0 or 1;
z = 0; j-m, v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 42E

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;

v-z = 0.



1. CMP-SA-PEG, α 2,8-ST

e-h = 1 to 4;

aa, bb, a-d, i, n-y (independently selected) = 0 or 1;

z = 0; j-m (independently selected) = 0 to 2;

v-y (independently selected) = 1,

when j-m (independently selected) is 2;

R = PEG.

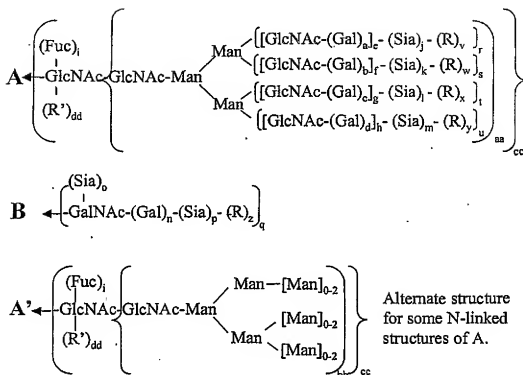
FIG. 42F

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2 peptides

A or A' - N-linked sites

B - O-linked sites



a-d, i, n-u, (independently selected) = 0 or 1.

aa, bb, cc, dd (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, .

glycoconjugate.

FIG. 42G

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;
dd, v-z = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
2. H_4N_2 -PEG

e-h = 1 to 4;

aa, bb, cc, a-d, i, n-u (independently selected) = 0 or 1;
dd, z = 0; j-m, v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 42H

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;
dd, v-z = 0.

- ↓
1. endo-H
2. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;
cc, v-z = 0; R' = -Gal-PEG.

FIG. 42I

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. ST3Gal3, CMP-SA
 2. endo-H
 3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;

cc, v-z = 0; R' = -Gal-PEG.

FIG. 42J

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. mannosidases
 2. GNT 1 & 2, UDP-GlcNAc
 3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;

bb, cc, dd, z = 0; R = PEG.

FIG. 42K

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;
dd, v-z = 0.

- ↓
1. mannosidases
 2. GNT-1, 2, 4 & 5; UDP-GlcNAc
 3. galactosyltransferase, UDP-Gal
 4. ST3Gal3, CMP-SA

e-h = 1 to 4;

aa, bb, cc, a-d, i, j-q (independently selected) = 0 or 1;
dd, v-z = 0.

FIG. 42L

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;
dd, v-z = 0.

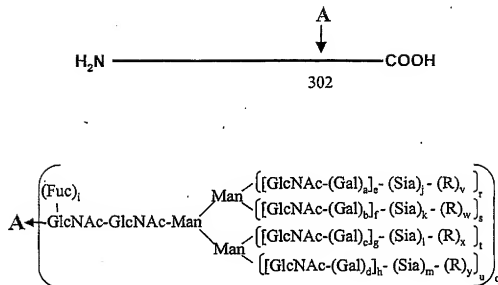
- ↓
1. mannosidases
 2. GNT-1, UDP-GlcNAc-PEG

e-h = 0 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;
bb, cc, dd, z = 0.

FIG. 42M

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 43A

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CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 43B

CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 43C

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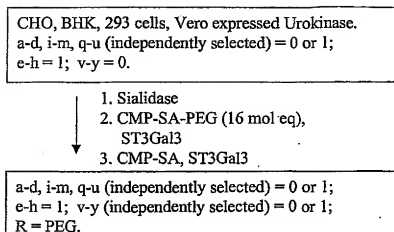


FIG. 43D

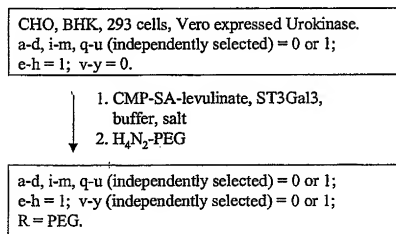


FIG. 43E

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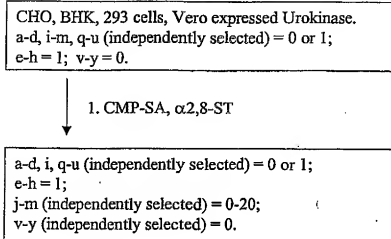
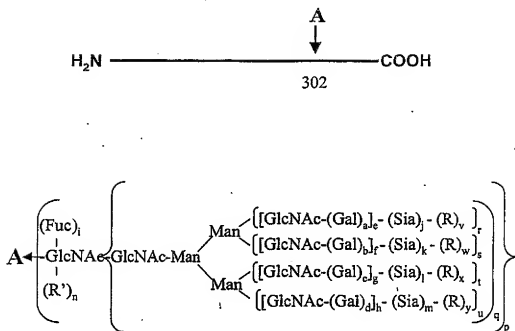


FIG. 43F

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 43G

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Insect cell expressed Urokinase.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-n = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 43H

Yeast expressed Urokinase.

a-n = 0;

q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 43I

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CHO, BHK, 293 cells, Vero expressed Urokinase.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; n, v-y = 0.

1. CMP-SA-linker-SA-CMP, ST3Gal3
2. ST3Gal1, desialylated Urokinase produced in CHO.
3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
 p = 1; n = 0;
 v-y (independently selected) = 0 or 1;
 R = linker-Urokinase.

FIG. 43J

Isolated Urokinase.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0; n = 0;
 Sia (independently selected) = Sia or SO₄;
 Gal (independently selected) = Gal or GalNAc;
 GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

1. sulfhydrylase
2. CMP-SA-PEG, sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;
 n = 0; e-h = 1; Sia = Sia;
 Gal (independently selected) = Gal or GalNAc;
 GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.
 v-y (independently selected) = 0 or 1;
 R = PEG.

FIG. 43K

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Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n = 0; v-y = 0;

Sia (independently selected) = Sia or SO₄;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.



1. sulfohydrolase, hexosaminidase

2. UDP-Gal-PEG, galactosyltransferase

a-d, i, q-u (independently selected) = 0 or 1;

e-h = 1; j-n = 0; Gal (independently selected) = Gal;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 43L

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CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 44B

CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq), ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 44C

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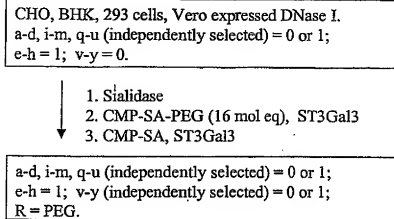


FIG. 44D

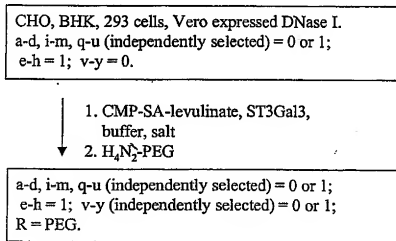


FIG. 44E

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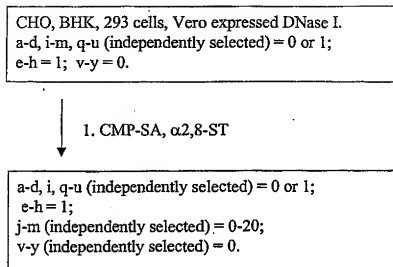
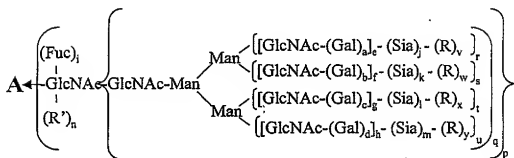
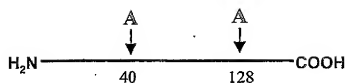


FIG. 44F

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 44G

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Insect cell expressed DNase I.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1; j-n = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 44H

Yeast expressed DNase I.

a-n = 0;

q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-n, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 44I

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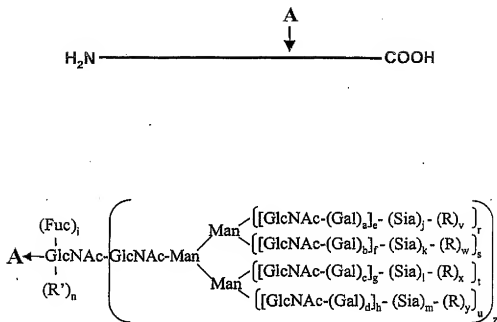
CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated alpha-1-Proteinase inhibitor.
 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker- alpha-1-Proteinase inhibitor.

FIG. 44J

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 45A

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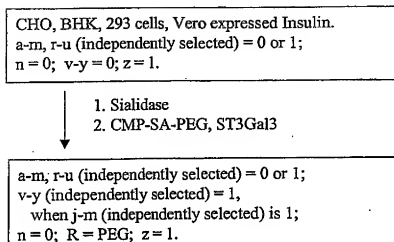


FIG. 45B

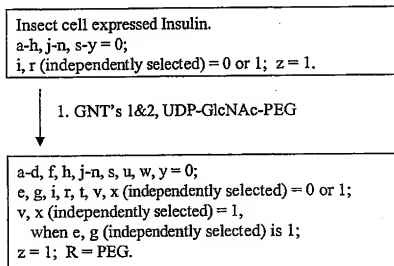


FIG. 45C

201/497

Yeast expressed Insulin.

a-n = 0; r-y (independently selected) = 0 to 1;

z = 1;

R (branched or linear) = Man, oligomannose or
polysaccharide.



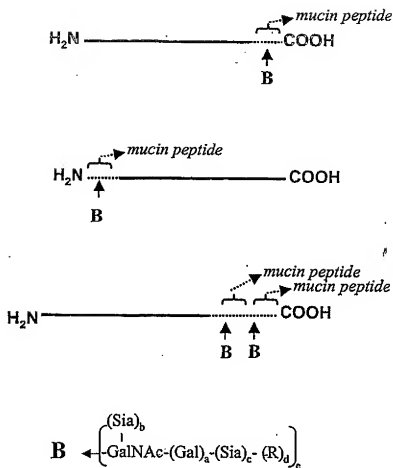
1. Endo-H

2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z = 0; n = 1; R' = -Gal-PEG.

FIG. 45D

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a-c, e (independently selected) = 0 or 1;
 d = 0; R = polymer

FIG. 45E

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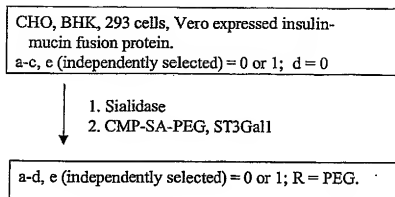


FIG. 45F

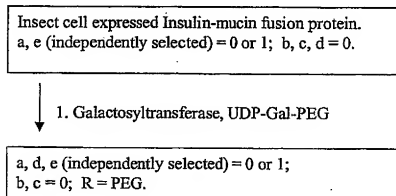


FIG. 45G

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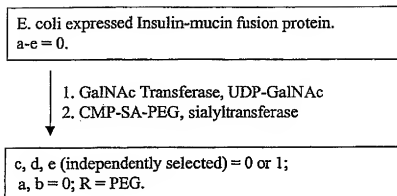
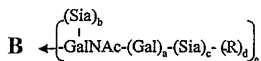
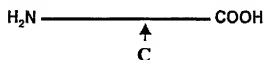
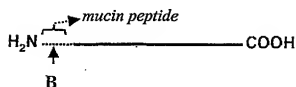


FIG. 45H

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a-c, e (independently selected) = 0 or 1;
 d = 0; R = modifying group, mannose,
 oligo-mannose.

FIG. 45I

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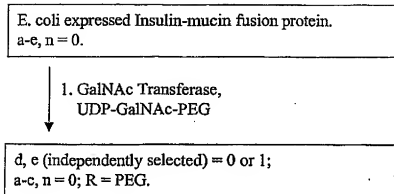


FIG. 45J

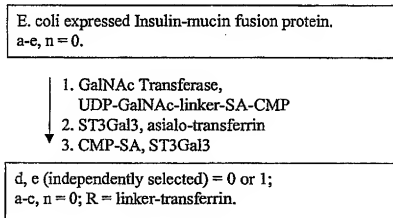


FIG. 45K

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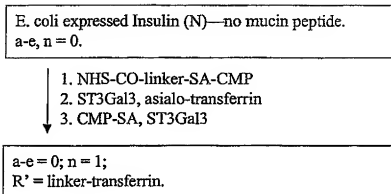
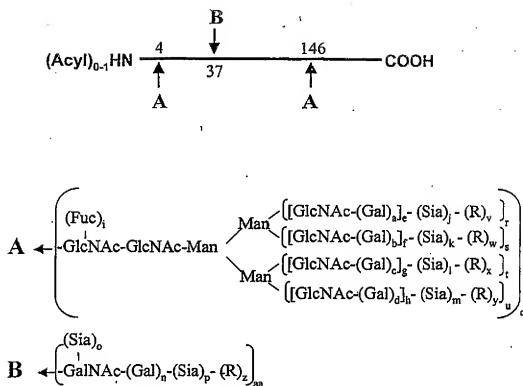


FIG. 45L

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a-d, i, n-u, aa (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 46A

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CHO, BHK, 293 cells, Vero expressed M-antigen.
 a-d, i-m, o-u, aa (independently selected) = 0 or 1;
 n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-linker-lipid-A,
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;
 o, p, z = 0; n, e-h = 1;
 v-y (independently selected) = 1,
 when j-m (independently selected) is 1;
 R = linker-lipid-A.

FIG. 46B

CHO, BHK, 293 cells, Vero expressed M-antigen.
 a-d, i-m, o-u, aa (independently selected) = 0 or 1;
 n, e-h = 1; v-z = 0.

- ↓
1. sialidase
 2. CMP-SA-linker-tetanus toxin, ST3Gal1
 3. CMP-SA, ST3Gal3

a-d, i-m, p-u, z, aa (independently selected) = 0 or 1;
 o, v-y = 0; n, e-h = 1; R = tetanus toxin.

FIG. 46C

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NSO expressed M-antigen.

a-d, i-n, o-u, aa (independently selected) = 0 or 1;

e-h = 1; v-z = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. α -galactosidase
 2. CMP-SA, ST3Gal3
 2. CMP-SA-KLH, ST3Gal1

a-d, i-n, p-u, z, aa (independently selected) = 0 or 1;

e-h = 1; o, v-y = 0;

z = 1, when p = 1;

R = KLH.

FIG. 46D

Yeast expressed M-antigen.

a-p, z = 0; q-y, aa (independently selected) = 0 to 1;

R (branched or linear) = Man, oligomannose;

GalNAc = Man.

- ↓
1. α 1,2-mannosidase
 2. GNT 1,
- ↓ UDP-GlcNAc-linker-diphtheria toxin.

e, q, l, m, r, t, u, v, aa (independently selected) = 0 or 1;

a-d, f-h, j, k, n-p, s, w-z = 0;

Sia = Man; R = linker-diphtheria toxin.

FIG. 46E

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CHO, BHK, 293 cells, Vero expressed M-antigen.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.



1. CMP-SA-levulinate, ST3Gal3,
2. H₄N₂-linker-DNA

a-d, i-m, o-y, aa (independently selected) = 0 or 1;
z = 0; n, e-h = 1; R = linker-DNA.

FIG. 46F

CHO, BHK, 293 cells, Vero expressed M-antigen.
a-d, i-n, o-u, aa (independently selected) = 0 or 1;
e-h = 1; v-z = 0.

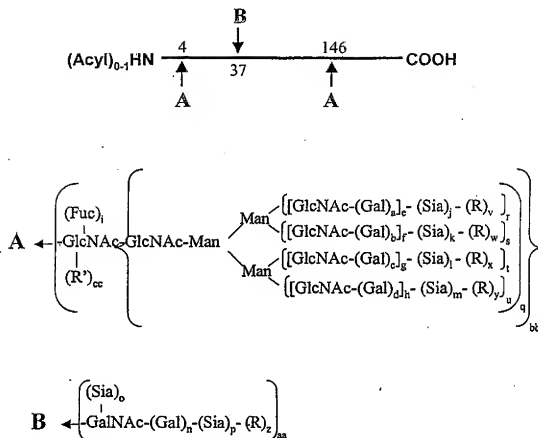


1. CMP-SA, poly- α 2,8-ST

a-d, i, n-u, aa (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-100;
v-z (independently selected) = 0.

FIG. 46G

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a-d, i, n, q-u, aa, bb, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-p (independently selected) = 0 to 100.

Cc, v-y = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 46H

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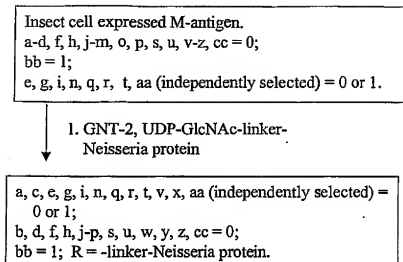


FIG. 46I

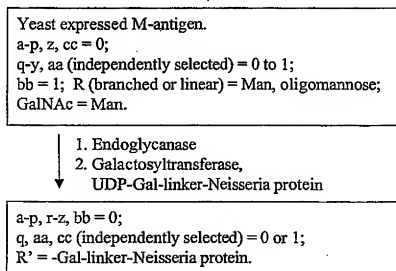


FIG. 46J

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Yeast expressed M-antigen.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1; bb = 1;

R (branched or linear) = Man, oligomannose;

GalNAc = Man.

1. mannosidases

2. GNT 1 & 2, UDP-GlcNAc

3. UDP-Gal, Galactosyltransferase,

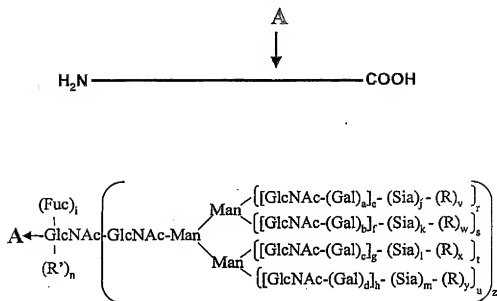
4. CMP-SA, sialyltransferase

a, c, e, g, j, l, q, r, t, aa (independently selected) = 0 or 1;

b, d, f, h, k, m-p, s, u-z, cc = 0; bb = 1.

FIG. 46K

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 47A

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CHO, BHK, 293 cells, Vero expressed Growth Hormone.

a-m, r-u (independently selected) = 0 or 1;
n = 0; v-y = 0; z = 1.

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3

a-m, r-u (independently selected) = 0 or 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
n = 0; R = PEG; z = 1.

FIG. 47B

Insect cell expressed growth hormone.

a-h, j-n, s-y = 0;
i, r (independently selected) = 0 or 1; z = 1.

- ↓
1. GNT's 1&2, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, w, y = 0;
e, g, i, r, t, v, x (independently selected) = 0 or 1;
v, x (independently selected) = 1,
when e, g (independently selected) is 1;
z = 1; R = PEG.

FIG. 47C

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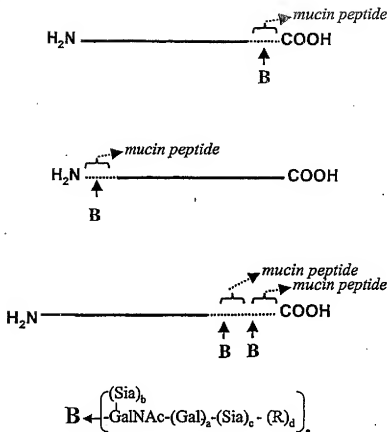
Yeast expressed growth hormone.
a-n = 0; r-y (independently selected) = 0 to 1;
z = 1;
R (branched or linear) = Man, oligomannose or
polysaccharide.

- ↓
1. Endo-H
2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z = 0; n = 1; R' = -Gal-PEG.

FIG. 47D

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a-c, e (independently selected) = 0 or 1;

d = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 47E

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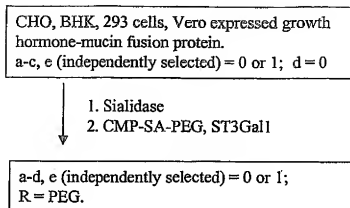


FIG. 47F

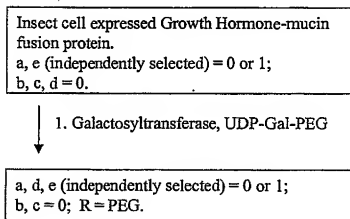


FIG. 47G

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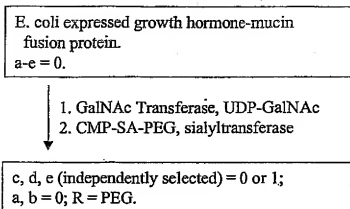


FIG. 47H

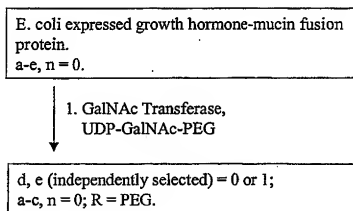


FIG. 47I

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E. coli expressed growth hormone-mucin fusion protein.

a-e, n = 0.

1. GalNAc Transferase,
UDP-GalNAc-linker-SA-CMP
2. ST3Gal3, asialo-transferrin
3. CMP-SA, ST3Gal3

d, e (independently selected) = 0 or 1;
a-c, n = 0; R = linker-transferrin.

FIG. 47J

E. coli expressed growth hormone
(N)—no mucin peptide.

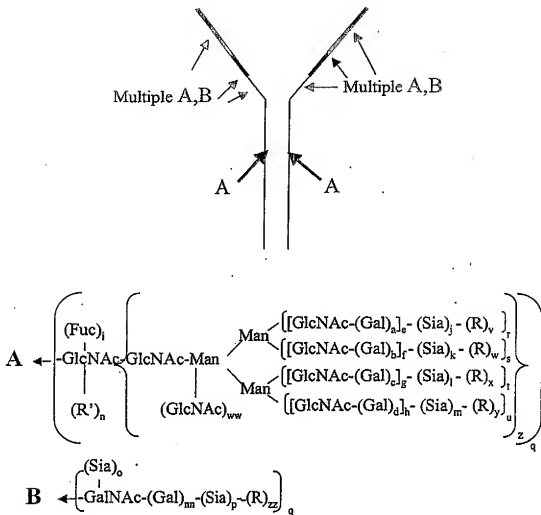
a-e, n = 0.

1. NHS-CO-linker-SA-CMP
2. ST3Gal3, asialo-transferrin
3. CMP-SA, ST3Gal3

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 47K

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a-d, i-m, q-u, w, z, nn, ww, zz (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

$$n, v-y = 0;$$

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 48A

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CHO, BHK, 293 cells, Vero or transgenic animals
expressed TNF Receptor IgG Fusion.
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. CMP-SA, ST3Gal1
 2. galactosyltransferase, UPD-Gal
 3. CMP-SA-PEG, ST3Gal3

a-m, o-u, v-y, aa (independently selected) = 0 or 1;
n = 1; z = 0; R = PEG.

FIG. 48B

CHO, BHK, 293 cells, Vero expressed
TNF Receptor IgG Fusion.
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. sialidase
 2. CMP-SA-PEG, ST3Gal1

a-i, p-u, z, aa (independently selected) = 0 or 1;
n = 1; o, j-m, v-y = 0; R = PEG.

FIG. 48C

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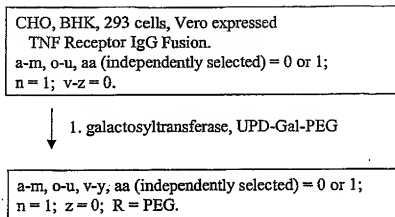


FIG. 48D

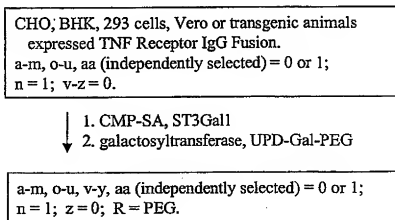


FIG. 48E

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CHO, BHK, 293 cells, Vero or transgenic animals
expressed TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

↓
1. CMP-SA-levulinate, ST3Gal1
2. H₄N₂-PEG

a-m, o-u, v-y, aa (independently selected) = 0 or 1;
n = 1; z = 0; R = PEG.

FIG. 48F

CHO, BHK, 293 cells, Vero expressed
TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

↓
1. CMP-SA-PEG, α2,8-ST

a-i, o, q-u, v-z, aa (independently selected) = 0 or 1;
n = 1; j-m, p (independently selected) = 0 to 2;
v-z (independently selected) = 1,
when j-m, p (independently selected) is 2;
R = PEG.

FIG. 48G

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CHO, BHK, 293 cells, Vero expressed Herceptin.

a, c, i (independently selected) = 0 or 1;

e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;

q, z = 1.



1. galactosyltransferase, UPD-Gal

2. CMP-SA-toxin, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;

e, g, r, t = 1; R = toxin;

f, h, k, m, n, s, u-y = 0; q, z = 1;

v-y (independently selected) = 51,

when j, l (independently selected) is 1.

FIG. 49B

CHO, BHK, 293 cells, Vero or fungal expressed Herceptin.

a, c, i (independently selected) = 0 or 1;

e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;

q, z = 1.



1. galactosyltransferase,

UPD-Gal-Toxin

a, c, i (independently selected) = 0 or 1;

e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;

q, z = 1; v-y (independently selected) = 1,

when a, c (independently selected) is 1;

R = toxin.

FIG. 49C

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Fungi expressed Herceptin.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

1. Endo-H

2. Galactosyltransferase, UDP-Gal

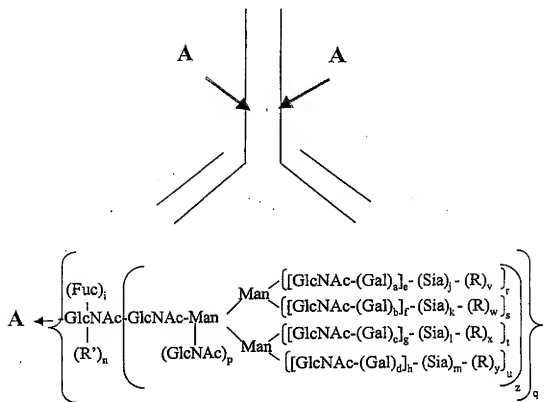
↓ 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 49D

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a-d, i, p-u, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 50A

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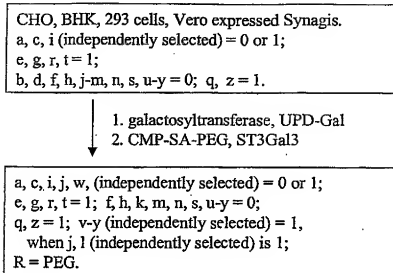


FIG. 50B

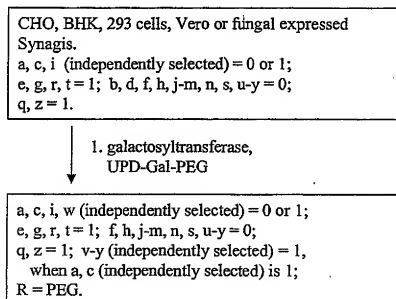


FIG. 50C

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Fungi expressed Synagis.

e, g, i, r, t (independently selected) = 0 or 1;

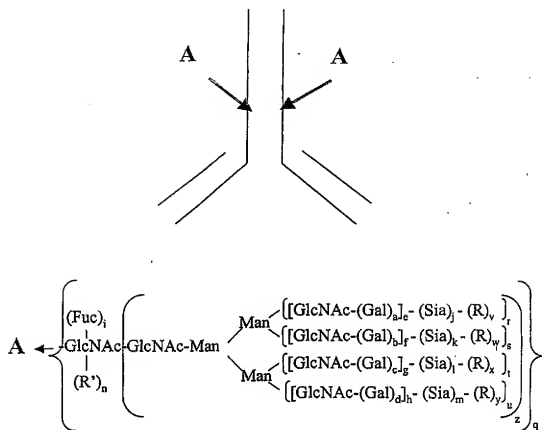
a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

- ↓
1. Endo-H
2. Galactosyltransferase, UDP-Gal
3.: CMP-SA-PEG, ST3Gal3

a-m, r-z = 0; q, n = 1; R' = -Gal-Sia-PEG.

FIG. 50D

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a-d, i, q-u, w (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 51A

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CHO, BHK, 293 cells, Vero expressed Remicade.
 a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
 q, z = 1.

- ↓
1. galactosyltransferase, UPD-Gal
 2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;
 e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;
 q, z = 1; v-y (independently selected) = 1,
 when j, l (independently selected) is 1;
 R = PEG.

FIG. 51B

CHO, BHK, 293 cells, Vero or fungal expressed
 Remicade.
 a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
 q, z = 1.

- ↓
1. galactosyltransferase,
UPD-Gal-PEG

a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;
 q, z = 1; v-y (independently selected) = 1,
 when a, c (independently selected) is 1;
 R = PEG.

FIG. 51C

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Fungi expressed Remicade.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

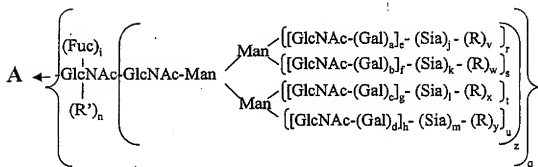
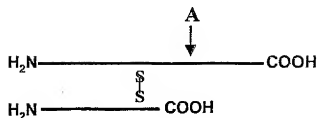
- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 51D

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 52A

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CHO, BHK, 293 cells, Vero expressed Reopro.
a-m, r-u (independently selected) = 0 or 1;
n = 0; v-y = 0; z = 1.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3

a-m, r-u (independently selected) = 0 or 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
n = 0; R = PEG; z = 1.

FIG. 52B

Insect cell expressed Reopro.
a-h, j-n, s-y = 0; i, r (independently selected) = 0 or 1;
z = 1.



1. GNT's 1&2, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, w, y = 0;
e, g, i, r, t, v, x (independently selected) = 0 or 1;
v, x (independently selected) = 1,
when e, g (independently selected) is 1;
z = 1; R = PEG.

FIG. 52C

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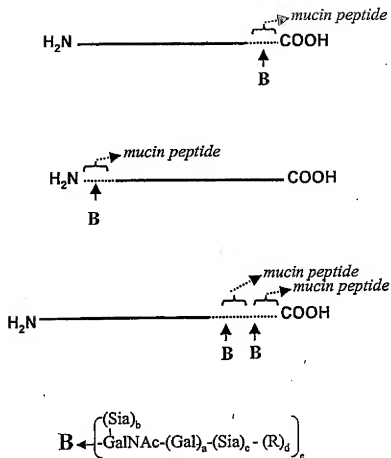
Yeast expressed Reopro.
a-n = 0; r-y (independently selected) = 0 to 1;
z = 1;
R (branched or linear) = Man, oligomannose or
polysaccharide.

- ↓
1. Endo-H
2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z = 0; n = 1; R' = -Gal-PEG.

FIG. 52D

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a-c, e (independently selected) = 0 or 1;
 d = 0; R = polymer

FIG. 52E

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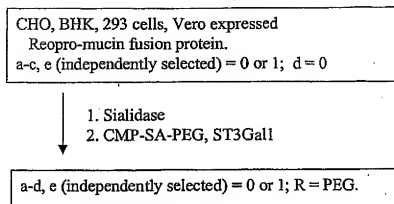


FIG. 52F

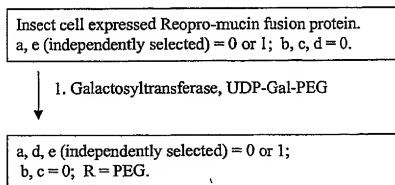


FIG. 52G

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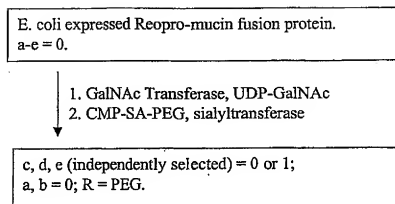
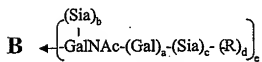
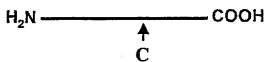
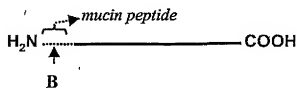
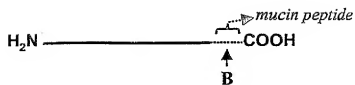


FIG. 52H

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a-c, e (independently selected) = 0 or 1;
d = 0; R = polymer, linker.

FIG. 52I

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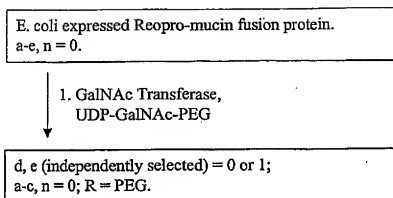


FIG. 52J

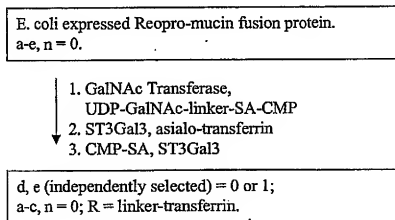


FIG. 52K

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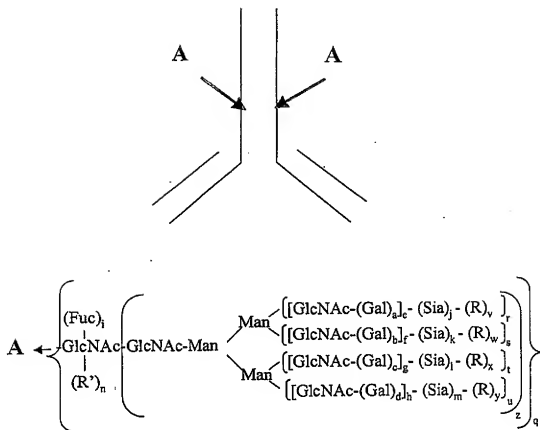
E. coli expressed Reopro(N)—no mucin peptide.
a-e, n = 0.

- ↓
1. NHS-CO-linker-SA-CMP
 2. ST3Gal3, asialo-transferrin
 3. CMP-SA, ST3Gal3

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 52L

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer, toxin, radioisotope-complex, drug, glycoconjugate.

R' = H, sugar, glycoconjugate.

z

FIG. 53A

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CHO, BHK, 293 cells, Vero or transgenic animal
expressed Rituxan.

a, c, i (independently selected) = 0 or 1;
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0; q, z = 1.



1. galactosyltransferase, UPD-Gal
2. CMP-SA-toxin, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;
e, g, r, t = 1;
f, h, k, m, n, s, u-y = 0; q, z = 1;
v-y (independently selected) = 1,
when j, l (independently selected) is 1;
R = toxin.

FIG. 53B

CHO, BHK, 293 cells, Vero or fungal expressed
Rituxan.

a, c, e, g, i, r, t (independently selected) = 0 or 1;
b, d, f, h, j-m, n, s, u-y = 0; q, z = 1.



1. galactosyltransferase,
UPD-Gal-drug

a, c, i (independently selected) = 0 or 1;
e, g, r, t = 1; f, h, j-m, n, s, u-y = 0; q, z = 1;
v-y (independently selected) = 1,
when a, c (independently selected) is 1;
R = toxin.

FIG. 53C

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Fungi expressed Rituxan.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

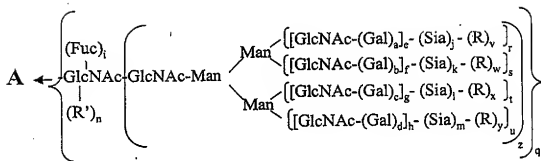
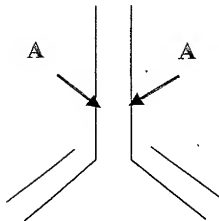
1. Endo-H
2. Galactosyltransferase, UDP-Gal
- ↓ 3. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 53D

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug,
glycoconjugate, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 53E

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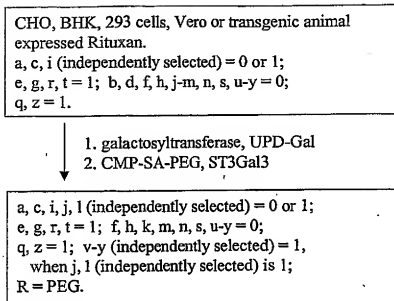


FIG. 53F

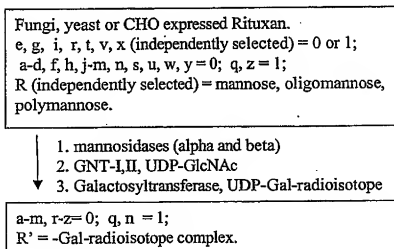
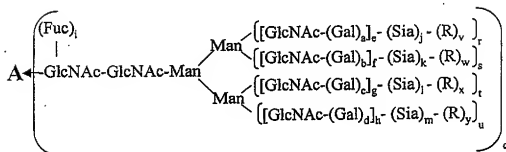
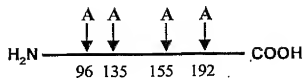


FIG. 53G

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a-d, i, q-u (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 100.
 v-y = 0; R = mannose, polymer.

FIG. 54A

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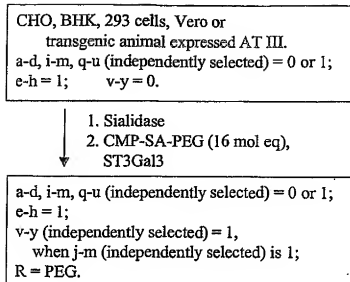


FIG. 54B

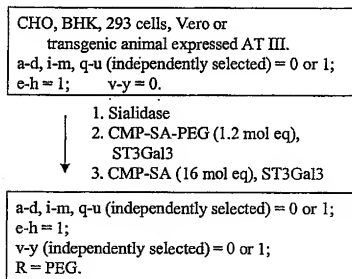


FIG. 54C

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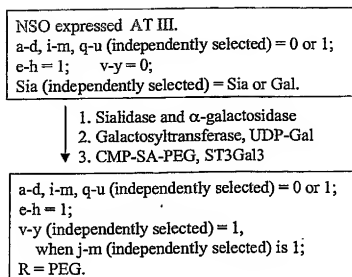


FIG. 54D

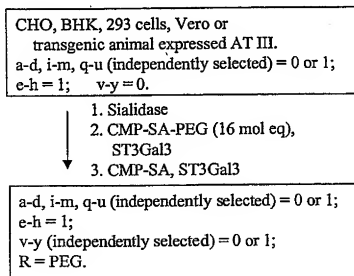


FIG. 54E

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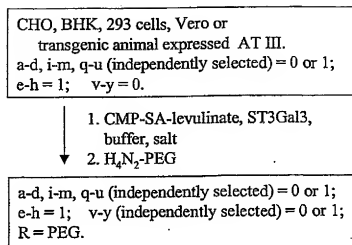


FIG. 54F

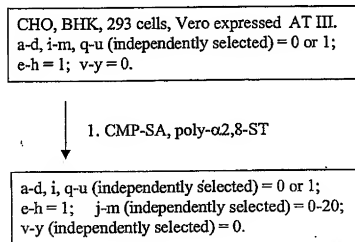
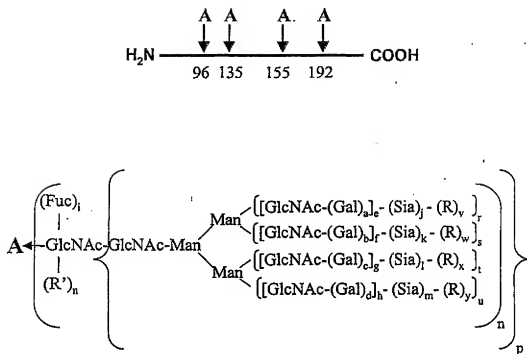


FIG. 54G

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a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100.

R = polymer, linker, mannose.

R' = H, sugar, glycoconjugate.

FIG. 54H

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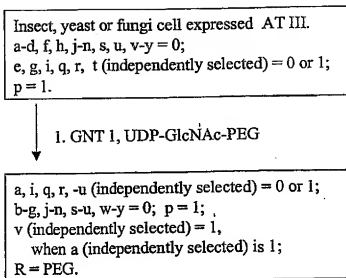


FIG. 54I

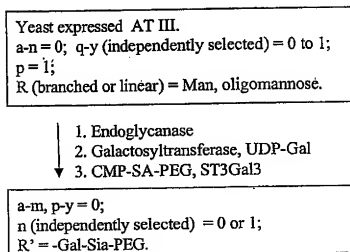


FIG. 54J

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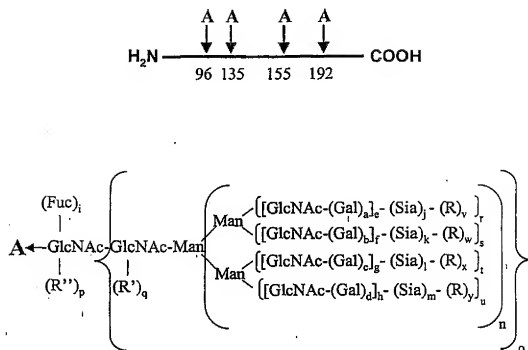
CHO, BHK, 293 cells, Vero expressed AT III.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, transferrin
treated with endoglycanase

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 54K

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer.

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 54L

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Yeast expressed AT III.

a-h, i-m, p, q = 0;

R (independently selected) = mannose,
oligomannose, polymannose;

r-u, v-y (independently selected) = 0 or 1;

n, o = 1.

↓ 1. endoglycanase

↓ 2. Galactosyltransferase, UDP-Gal-PEG

a-h, i-o, q, r-u, v-y = 0; p = 1.

R'' = Gal-PEG.

FIG. 54M

Plant expressed AT III.

a-d, f-h, j-m, p, s-u, v-y = 0;

e, i, q, r (independently selected) = 0 or 1;

n, o = 1; R' = xylose.

↓ 1. xylosidase

↓ 3. Galactosyl transferase, UDP-
Gal-PEG

b-d, f-h, j-m, p, q, s-u, w-y = 0;

a, e, i, r (independently selected) = 0 or 1;

n, o = 1; R = PEG.

FIG. 54N

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CHO, BHK, 293 cells, Vero, transgenic animal
expressed AT III.

a-h, i-o, r-u (independently selected) = 0 or 1;

p, q, v-y = 0.



1. CMP-SA-PEG,
ST3Gal3

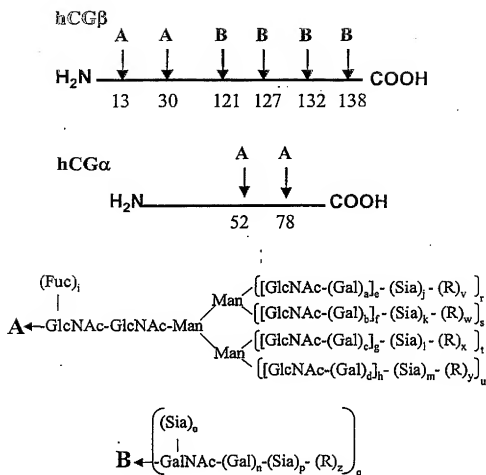
a-h, i-o, r-u (independently selected) = 0 or 1;

p, q = 0; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 54O

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0; R = polymer

FIG. 55A

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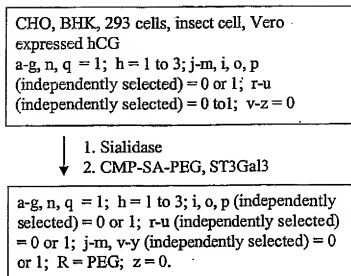


FIG. 55B

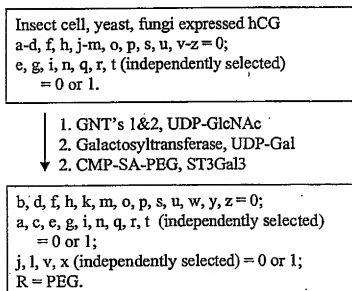


FIG. 55C

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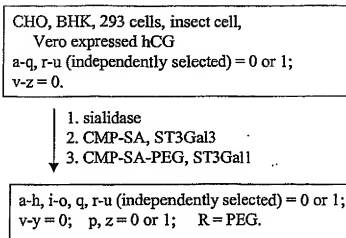


FIG. 55D

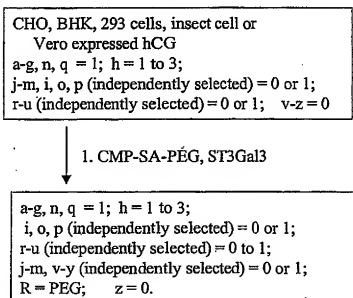


FIG. 55E

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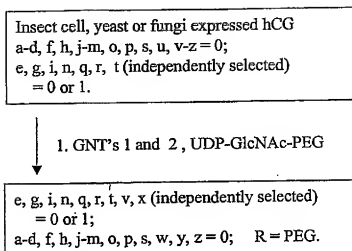


FIG. 55F

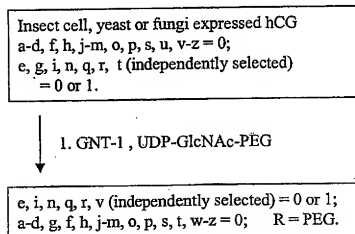


FIG. 55G

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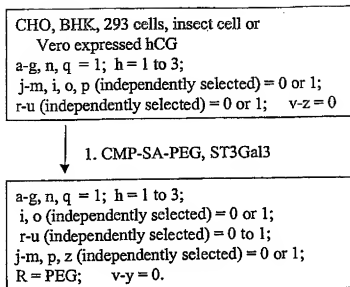


FIG. 55H

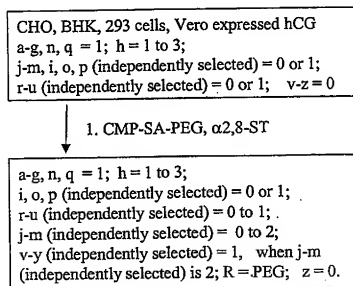


FIG. 55I

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CHO, BHK, 293 cells, Vero expressed hCG
a-g, n, q = 1; h = 1 to 3;
j-m, i, o, p (independently selected) = 0 or 1;
r-u (independently selected) = 0 to 1; v-z = 0

↓
1. CMP-SA, poly- α 2,8-ST

a-i, j-q, r-u, (independently selected) = 0 or 1;
v-z (independently selected) = 0-100; R = Sia.

FIG. 55J

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CHO, BHK, 293 cells, insect cells, Vero expressed and secreted alpha-galactosidase
 a-h, i-m, q-u (independently selected) = 0 or 1;
 z = 1; n, v-y = 0; and when a-n = 0, then r-u (independently selected) = 0 or 1; v-y (independently selected) = 0-100;
 R = mannose or mannose with mannose-6-phosphate.

- ↓
 1. Endo-H
 2. Galactosyltransferase, UDP-Gal-PEG-transferrin

a-h, i-m, q-u (independently selected) = 0 or 1;
 n, v-y = 0; z = 1; and when z = 0 and q = 1,
 then n (independently selected) = 0 or 1;
 R' = Gal-PEG-transferrin.

FIG. 56B

CHO, BHK, 293 cells, Insect cells,
 Vero expressed and secreted alpha-galactosidase
 a-h, i-m, q-u (independently selected) = 0 or 1; z = 1; n, v-y = 0; and when a-n = 0, then r-u (independently selected) = 0 or 1; v-y (independently selected) = 0-100;
 R = mannose or mannose with mannose-6-phosphate.

- ↓
 1. Sialidase
 2. CMP-SA-linker-Mannose-6-phosphate
 ST3Gal3

a-h, i-m, q-u, v-y (independently selected) = 0 or 1;
 n = 0; z = 1; R = mannose-6-phosphate; and when a-n = 0, then r-u (independently selected) = 0 or 1;
 v-y (independently selected) = 0-100;
 R = mannose or mannose with mannose-6-phosphate.

FIG. 56C

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NSO expressed alpha-galactosidase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

1. Sialidase and α -galactosidase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-linker-mannose-6-phosphate
sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1; e-h = 1;
v-y (independently selected) = 1, when j-m (independently
selected) is 1; R = mannose-6 phosphate

FIG. 56D

CHO, BHK, 293 cells, Insect cells, Vero expressed and
secreted alpha-galactosidase

a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;

n, v-y = 0; and when a-n = 0, then r-u (independently
selected) = 0 or 1; v-y (independently selected) = 0-100;

R = mannose or mannose with mannose-6-phosphate.

1. Sialidase
2. CMP-SA-PEG, sialyltransferase

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0; z
= 1; R = PEG; and when a-n = 0, then r-u (independently
selected) = 0 or 1; v-y = 0-100; R = mannose or mannose
with mannose-6-phosphate.

FIG. 56E

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CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi
expressed alpha-galactosidase.
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. mannosyltransferase,
GDP-mannose-linker-ApoE

a-i = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate;
v-y (independently selected) = 0 or 1;
R = mannose-linker-ApoE.

FIG. 56F

CHO, BHK, 293 cells, Insect cells, Vero, yeast,
fungi expressed alpha-galactosidase.
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. endo-H
2. galactosyltransferase,
UDP-Gal-linker-alpha2-macroglobulin

a-m, r-z = 0; n, q (independently selected) = 0 or 1;
R' = galactose-linker-alpha2-macroglobulin.

FIG. 56G

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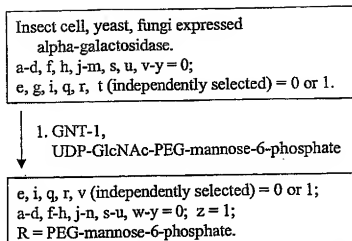


FIG. 56H

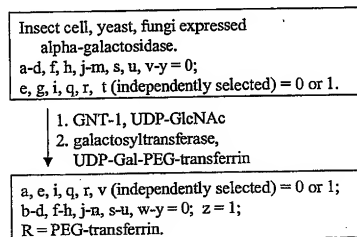


FIG. 56I

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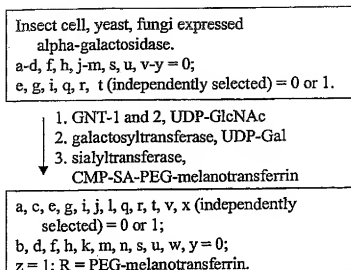
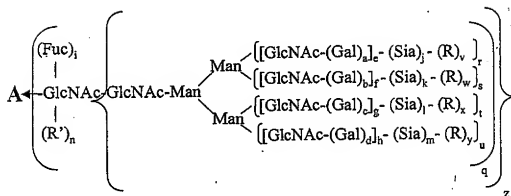
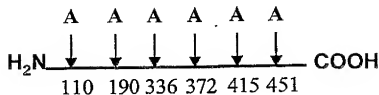


FIG. 56J

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a-d, i, n, q-u, z (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100;

R = mannose, mannose-6-phosphate and mannose, polymer.

FIG. 57A

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CHO, BHK, 293 cells, Insect cells, Vero expressed
and secreted alpha-iduronidase

a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;
n, v-y = 0; and when a-n = 0, then r-u (independently
selected) = 0 or 1; v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Endo-H
2. Galactosyltransferase, UDP-Gal-PEG-transferrin

a-h, i-m, q-u (independently selected) = 0 or 1;
n, v-y = 0; z = 1; and when z = 0 and q = 1, then n
(independently selected) = 0 or 1; R' = Gal-PEG-transferrin.

FIG. 57B

CHO, BHK, 293 cells, Insect cells, Vero expressed
and secreted alpha-iduronidase

a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;
n, v-y = 0; and when a-n = 0, then r-u (independently
selected) = 0 or 1; v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
2. CMP-SA-linker-Mannose-6-phosphate ST3Gal3

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0;
z = 1; R = mannose-6-phosphate; and when a-n = 0,
then r-u (independently selected) = 0 or 1;
v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

FIG. 57C

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NSO expressed alpha-iduronidase.

a-d, i-m, q-u (independently selected) = 0 or 1; e-h = 1;
v-y = 0; Sia (independently selected) = Sia or Gal.

1. Sialidase and α -galactosidase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-linker-mannose-6-phosphate sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = mannose-6 phosphate

FIG. 57D

CHO, BHK, 293 cells, Insect cells, Vero expressed
and secreted alpha-iduronidase

a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;
n, v-y = 0; and when a-n = 0, then r-u (independently
selected) = 0 or 1; v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

1. Sialidase
2. CMP-SA-PEG, sialyltransferase

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0;
z = 1; R = PEG; and when a-n = 0, then r-u
(independently selected) = 0 or 1; v-y = 0-100;
R = mannose or mannose with mannose-6-phosphate.

FIG. 57E

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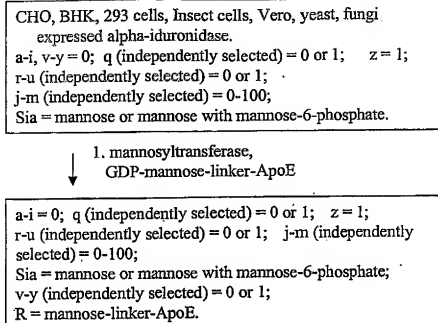


FIG. 57F

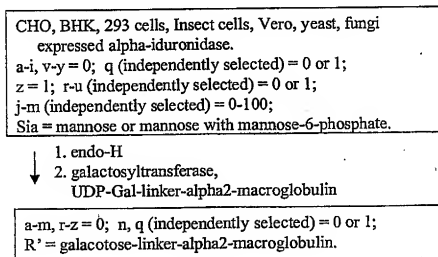


FIG. 57G

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Insect cell, yeast, fungi expressed
 alpha-iduronidase.
 a-d, f, h, j-m, s, u, v-y = 0;
 e, g, i, q, r, t (independently selected) = 0 or 1.

↓ 1. GNT-1,
 UDP-GlcNAc-PEG-mannose-6-phosphate

e, i, q, r, v (independently selected) = 0 or 1;
 a-d, f-h, j-n, s-u, w-y = 0; z = 1;
 R = PEG-mannose-6-phosphate.

FIG. 57H

Insect cell, yeast, fungi expressed
 alpha-iduronidase.
 a-d, f, h, j-m, s, u, v-y = 0;
 e, g, i, q, r, t (independently selected) = 0 or 1.

↓ 1. GNT-1, UDP-GlcNAc
 2. galactosyltransferase,
 UDP-Gal-PEG-transferrin

a, e, i, q, r, v (independently selected) = 0 or 1;
 b-d, f-h, j-n, s-u, w-y = 0; z = 1;
 R = PEG-transferrin.

FIG. 57I

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Insect cell, yeast, fungi expressed
alpha-iduronidase.

a-d, f, h, j-m, s, u, v-y = 0;

c, g, i, q, r, t (independently selected) = 0 or 1.

1. GNT-1 and 2, UDP-GlcNAc

2. galactosyltransferase, UDP-Gal

↓ 3. sialyltransferase,

CMP-SA-PEG-melanotransferrin

a, c, e, g, i, j, l, q, r, t, v, x

(independently selected) = 0 or 1;

b, d, f, h, k, m, n, s, u, w, y = 0; z = 1;

R = PEG-melanotransferrin.

FIG. 57J

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FIG. 58A

ACCCCCCTGGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCTGCTCAAT
GCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAG
GAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCCAGGAGCTGGT
GCTGCTCGGACACTCTCTGGGCATCCCCCTGGGCTCCCCTGAGCAGCTG
CCCCAGCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATA
GCGGCCTTTTCTCTACCAGGGGCTCCTGCAGGGCCCTGGAAGGGATCT
CCCCCGAGTTGGGTCCACCTTGGACACACTGCAGCTGGACGTCGCCG
ACTTTGCCACCACCATCTGGCAGCAGATGGAAGAAGCTGGGAATGGCC
CCTGCCCTGCAGCCACCCAGGGTGCCATGCCGCCCTTCGCCTCTGCT
TTCCAGCGCCGGGCAGGAGGGGTCTGGTTGCCTCCCATCTGCAGAG
CTTCTGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAGCCCTG
A

FIG. 58B

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr
Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe
Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His
Leu Ala Gln Pro

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FIG. 59A

GC GCCTCTTATGTACCCACAAAAATCTATTTTCAAAAAAGTTGCTCTA
AGAAATATAGTTATCAAGTTAAGTAAAAATGTCAATAGCCTTTTAATTTA
ATTTTAAATTGTTTTATCATTCTTTGCAATAATAAACATTAACCTTTAT
ACTTTTAAATTTAATGTATAGAATAGAGATATACATAGGATATGTAAA
TAGATACACAGTGTATATGTGATTAAAAATATAATGGGAGATTCAATC
AGAAAAAAGTTTTCTAAAAAGGCTCTGGGGTAAAAGAGGAAAGGAAAC
AATAATGAAAAAAATGTGGTGAGAAAAACAGCTGAAAACCCATGTGA
AAGAGTGTATAAAGAAAGCAAAAAGAGAAAGTAGAAAGTAACACAGG
GGCATTGGA AAAATGTAAACGAGTATGTTCCCTATTTAAGGCTAGGC
ACAAAGCAAGGTCTTCAGAGAACCTGGAGCCTAAGGTTTAGGCTCAC
CCATTTCAACCAGTCTAGCAGCATCTGCAACATCTACAATGGCCTTGA
CCTTTGCTTTACTGGTGGCCCTCCTGGTGCTCAGCTGCAAGTCAAGCT
GCTCTGTGGGCTGTGATCTGCCTCAAACCCACAGCCTGGGTAGCAGG
AGGACCTTGATGCTCCTGGCACAGATGAGGAGAATCTCTCTTTCTCC
TGCTTGAAGGACAGACATGACTTTGGATTTCCCAGGAGGAGTTGG
CAACCAGTTC AAAAAGGCTGAAACCATCCCTGTCCTCCATGAGATGA
TCCAGCAGATCTTCAATCTCTTCAGCACAAAGGACTCATCTGCTGCTT
GGGATGAGACCCCTCCTAGACAAATTTCACTGAACTCTACCAGCAG
CTGAATGACCTGGAAGCCTGTGTGATACAGGGGGTGGGGGTGACAGA
GACTCCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGGAAATACT
TCCAAAGAATCACTCTCTATCTGAAAGAGAAGAAATACAGCCCTTG
GCCTGGGAGGTTGTGACAGCAGAAATCATGAGATCTTTTCTTTGTCA
ACAAACTTGCAAGAAAGTTTAAGAAAGTAAGGAATGAAAACCTGGTTCA
ACATGGAAATGATTTTCATTGATTTCGATGCCAGCTCACCTTTTATG
ATCTGCCATTTCAAAGACTCATGTTTCTGCTATGACCATGACACGATT
TAAATCTTTTCAAATGTTTTAGGAGTATTAATCAACATTGTATTGAG
CTCTTAAGGCACTAGTCCCTTACAGAGGACCATGCTGACTGATCCATT
ATCTATTTAAATATTTTTAAAAATATTATTTAITTAACATTTATAAAAC
AACTATTTTTGTTTCATATTATGTCATGTGCACCTTTGCACAGTGGTTA
ATGTAATAAAATGTGTTCTTTGTATTTGGTAAATTTATTTTGTGTTGTT
CATTGAACTTTTGCTATGGAACCTTTTGTACTTGTTTATTCTTTAAAAATG
AAATTCGAAGCCTAATTTGTGCAACCTGATTACAGAATAACTGGTACA
CTTCAATTTGTCCATCAATATTATATTCAAGATATAAGTAAAAATAAAC
TTTCTGTAAACCAAGTTGTATGTTGTACTCAAGATAACAGGGTGAACG
TAACAAATACAATTCTGCTCTCTGTGTATTTGATTTTGTATGAAAA
AACTAAAAATGGTAATCACTTAATTATCAGTTATGGTAAATGGT
ATGAAGAGAAGAAGGAACG

FIG. 59B

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Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys Lys Ser
 Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr
 Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln Lys Ala
 Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr
 Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu
 Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
 Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe
 Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val
 Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser Leu
 Arg Ser Lys Glu

FIG. 59C

ATGGCCCTCCTGTTCCCTCTACTGGCAGCCCTAGTGATGACCAGCTAT
 AGCCCTGTTGGATCTCTGGGCTGTGATCTGCCTCAGAACCATGGCCCTA
 CTTAGCAGGAACACCTTGGTGCTTCTGCACCAAATGAGGAGAATCTCC
 CCTTCTTGTGTCTCAAGGACAGAAGAGACTTCAGGTTCCTCCAGGAG
 ATGGTAAAAGGGAGCCAGTTGCAGAAGGCCCATGTCATGTCTGTCTCT
 CCATGAGATGCTGCAGCAGATCTTCAGCCTCTTCCACACAGAGCGCTC
 CTCGTCTGCCTGGAACATGACCCTCCTAGACCAACTCCACACTGGACT
 TCATCAGCAACTGCAACACCTGGAGACCTGCTTGCTGCAGGTAGTGG
 GAGAAGGAGAATCTGCTGGGGCAATTAGCAGCCCTGCCTGACCTTG
 AGGAGGTACTTCCAGGGAATCCGTGTCTACCTGAAAGAGAAGAAATA
 CAGCGACTGTGCCTGGGAAGTTGTCAGAATGGAAATCATGAAATCCT
 TGTTCCTATCAACAAACATGCAAGAAAGACTGAGAAGTAAAGATAGA
 GACCTGGGCTCATCTTGA

FIG. 59D

Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr Ser Pro Val
 Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg Asn Thr
 Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu Cys Leu Lys Asp
 Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val Lys Gly Ser Gln Leu Gln Lys
 Ala His Val Met Ser Val Leu His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His
 Thr Glu Arg Ser Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr
 Gly Leu

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FIG. 60A

ATGACCAACAAGTGCTCTCCTCCAAATTGCTCTCCTGTTGTGCTTCTCC
 ACTACAGCTCTTTCCATGAGCTACAACCTTGCTTGGATTCTACAAAAGA
 AGCAGCAATTTTCAGTGTGAGAAGCTCCTGTGGCAATTGAATGGGAG
 GCTTGAATATTGCCTCAAGGACAGGATGAACCTTGACATCCCTGAGG
 AGATTAAGCAGCTGCAGCAGTTCCAGAAGGAGGACGCCGCGATTGACC
 ATCTATGAGATGCTCCAGAACATCTTTGCTATTTTCAGACAAGATTCA
 TCTAGCACTGGCTGGAATGAGACTATTGTTGAGAACCTCCTGGCTAA
 TGTCTATCATCAGATAAACCATCTGAAGACAGTCCTGGAAGAAAAAC
 TGGAGAAAGAAGATTTTACCAGGGGAAAACTCATGAGCAGTCTGCGAC
 CTGAAAAGATATTATGGGAGGATTCTGCATTACCTGAAGGCCAAGGA
 GTACAGTCACTGTGCCTGGACCATAGTCAGAGTGGAAATCCTAAGGA
 ACTTTTACTTCATTAAACAGACTTACAGGTTACCTCCGAAACTGAAGAT
 CTCCTAGCCTGTCCCCTCTGGGACTGGACAATTGCTTCAAGCATTCTC
 AACCAGCAGATGCTGTTTAAAGTGACTGATGGCTAATGTACTGCAAAT
 GAAAGGACACTAGAAGATTTTGAATTTTTATTAAATTATGAGTTATT
 TTTATTAT TAAATTTTATTTTGGAAAAATAAATTATTTTGGTGC

FIG. 60B

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser Thr Thr Ala
 Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
 Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp
 Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln Phe Gln Lys Glu
 Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln
 Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp
 Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile
 Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val
 Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn

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FIG. 61A

ATGGTCTCCCAGGCCCTCAGGCTCCTCTGCCTTCTGCTTGGGCTTCAG
GGCTGCCTGGCTGCAGTCTTCGTAACCCAGGAGGAAGCCCACGGCGT
CCTGCACCGGCGCCGGCGGCCAACGCGTTCTTGGAGGAGCTGCGGC
CGGGCTCCCTGGAGAGGGAGTGCAAGGAGGAGCAGTGCTCCTTCGA
GGAGGCCCGGAGATCTTCAAGGACGCGGAGAGGACGAAGCTGTTC
TGGATTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCA
GAATGGGGGCTCCTGCAAGGACCAGTCCAGTCCATATCTGCTTCT
GCCTCCCTGCCTTCGAGGGCCGGAAGTGTGAGACGCACAAGGATGAC
CAGCTGATCTGTGTGAACGAGAACGCGGCTGTGAGCAGTACTGCAG
TGACCACACGGGCACCAAGCGCTCCTGTCCGTGCCACGAGGGGTACT
CTCTGCTGGCAGACGGGGTGTCTGCACACCCACAGTTGAATATCCA
TGTGGA AAAATACCTATTCTAGAAAAAAGAAATGCCAGCAAAACCCA
AGGCCGAATTGTGGGGGGCAAGGTGTGCCCAAAGGGGAGTGTCCA
TGGCAGGTCTCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGGGGGAC
CCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAA
AATCAAGAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGAC
CTCAGCGAGCACGACGCGGGATGAGCAGAGCCGCGGGTGGCGCAGG
TCATCATCCCCAGCACGTACGTCCCGGGCACCACCAACCACGACATC
GCGCTGTCTCCGCTGCACCAGCCGTGGTCTCTCACTGACCATGTGGTG
CCCCTCTGCCTGCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTC
GTGCGCTTCTCATTGGTACGCGCTGGGGCCAGCTGCTGGACCGTGG
CGCCACGGCCCTGGAGCTCATGGTGCTCAACGTGCCCCGGCTGATGA
CCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGGAGACTCCCCAAAT
ATCAGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA
CTCCTGCAAGGGGGACAGTGGAGGCCACATGCCACCACTACCGGG
GCACGTGGTACCTGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCA
ACCGTGGGCCACTTGGGGTGTACACCAGGGTCTCCAGTACATCGA
GTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCCAGGAGTCTCTC
TGCGAGCCCCATTCCC

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FIG. 61B

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln Gly Cys
Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val Leu His Arg Arg Arg
Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg
Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys
Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val
Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg
Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro
Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys
Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln
Val Leu Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile
Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg
Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp
Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro Leu
Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser
Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu
Met Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg
Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp
Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg
Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly
His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met
Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro

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FIG. 62A

ATGCAGCGCGTGAACATGATCATGGCAGAATCACC AAGCCTCATCAC
CATCTGCCTTTTAGGATATCTACTCAGTGCTGAATGTACAGTTTCTT
GATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAA
TTCAGGTAAATTGGAAGAGTTTGTTC AAGGGAACCTTGAGAGAGAAT
GTATGGAAGAAAAGTGTAGTTTTGAAGAACCACGAGAAGTTTTTGAA
AACTGAAAAGACAACCTGAATTTTGAAGCAGTATGTTGATGGAGA
TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATG
ACATTAATTCCTATGAATGTTGGTGCCCTTTGGATTTGAAGGAAAAGA
ACTGTGAATTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAG
CAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTACT
GAGGGATATCGACTTGCGAGAAAACCAGAAGTCCTGTGAACCAGCAGT
GCCATTTCCATGTGGGAAGAGTTCTGTTCACAAACTTCTAAGCTCAC
CCGTGCTGAGGCTGTTTTTCTGATGTGGACTATGTAATCCTACTGA
AGCTGAAACCATTTTGATAACATCACTCAAGGCACCCAATCATTTA
ATGACTTCACTCGGGTTGTTGGTGGAGAAGATGCCAAACCAGGTCAA
TTCCCTTGGCAGGTTGTTTGAATGGTAAAGTTGATGCATTCTGTGGA
GGCTCTATCGTTAATGAAAAATGGATTGTAAC TGCTGCCCACTGTGTT
GAAACTGGTGTTAAATACAGTTGTGCGCAGGTGAACATAATATTGA
GGAGACAGAACATACAGAGCAAAAGCGAAATGTGATTCGAGCAATT
ATTCTCACCACTACAATGCAGCTATTAATAAGTACAACCATGA
CATTGCCCTTCTGGAAC TGGACGAACCCCTTAGTGCTAAACAGCTACG
TTACACCTATTTGCATTGCTGACAAGGAATACACGAACATCTTCTCA
AATTTGGATCTGGCTATGTAAGTGGCTGGGCAAGAGTCTTCCACAAA
GGGAGATCAGCTTTAGTTCTCAGTACCTTAGAGTTCCACTTGTTGAC
CGAGCCACATGTCTTCGATCTACAAAGTTCACCATCTATAACAACAT
GTTCTGTGCTGGCTTCCATGAAGGAGGTAGAGATTCATGTCAAGGAG
ATAGTGGGGGACCCCATGTTACTGAAGTGGAAGGGACCAAGTTTCTTA
ACTGGAATTATTAGCTGGGGTGAAGAGTGTGCAATGAAAGGCAAAATA
TGGAATATATACCAAGGTATCCCGGTATGTCAACTGGATTAAGGAAA
AAACAAAGCTCACTTAATGAAAGATGGATTTC AAGGTTAATTCATT
GGAATTGAAAATTAACAG

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FIG. 62B

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr Ile Cys Leu
Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu Asp His Glu Asn Ala
Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn Ser Gly Lys Leu Glu Glu Phe
Val Gln Gly Asn Leu Glu Arg Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu
Pro Arg Glu Val Phe Glu Asn Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr
Val Asp Gly Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys
Asp Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn
Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe Cys
Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly Tyr Arg Leu
Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe Pro Cys Gly Arg Val Ser
Val Ser Gln Thr Ser Lys Leu Thr Arg Ala Glu Ala Val Phe Pro Asp Val Asp Tyr
Val Asn Pro Thr Glu Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser
Phe Asn Asp Phe Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe
Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile Val
Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly Val Lys Ile Thr
Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu His Thr Glu Gln Lys Arg Asn
Val Ile Arg Ala Ile Ile Pro His His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn
His Asp Ile Ala Leu Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr
Pro Ile Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu Val Leu Gln
Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg Ser Thr Lys Phe
Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His Glu Gly Gly Arg Asp Ser
Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Glu Val Glu Gly Thr Ser Phe Leu
Thr Gly Ile Ile Ser Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr
Thr Lys Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr

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FIG. 63A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTGCG
GTGTTTCTGTCATGTTCTCCATTCGGCTCCTGATGTGCAGGATTGCCCA
GAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCC
AATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCCTCC
ACTAAGGTCCAAGAAGACGATGTGGTCCAAAAGAACGTACCTCAG
AGTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATG
GGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTG
TTATTATCACAAATCTTAAATGTTTTACCAAGTGCTGTCTTGATGACT
GCTGATTTCTGGAATGGAAAATTAAGTTGTTTAGTGTTTATGGCTTT
GTGAGATAAAACTCTCCTTTTCCTTACCATAACCACTTTGACACGCTTC
AAGGATATACTGCAGCTTTACTGCCTTCTCCTTATCCTACAGTACAA
TCAGCAGTCTAGTTCTTTTCATTTGGAATGAATACAGCATTAAAGCTTG
TTCCACTGCAAAATAAGCCTTTTAAATCATC

FIG. 63B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His
Lys Ser

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FIG. 63C

ATGAAGACACTCCAGTTTTTTCTTCTCTTTTCTGTTGCTGGAAGCAATC
TGCTGCAATAGCTGTGAGCTGACCAACATCACCATTGCAATAGAGAA
AGAAGAATGTCGTTTTCTGCATAAGCATCAACACCACTTGGTGTGCTG
GCTACTGCTACACCAGGGATCTGGTGTATAAGGACCCAGCCAGGCC
AAAAATCCAGAAAACATGTACCTTCAAGGAACTGGTATATGAAACAGT
GAGAGTGCCCGGCTGTGCTCACCATGCAGATTCTTGTATACATACCC
AGTGGCCACCCAGTGTCACTGTGGCAAGTGTGACAGCGACAGCACTG
ATTGTACTGTGCGAGGCCTGGGGCCAGCTACTGCTCCTTTGGTGAAA
TGAAAGAATAA

FIG. 63D

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile Cys Cys
Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg Phe
Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp Leu Val
Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val
Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr
Pro Val Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys Glu

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FIG. 64A

CCCGGAGCCGGACCGGGGCCACCGCGCCGCTCTGCTCCGACACCGC
GCCCCCTGGACAGCCGCCCTCTCCTCCAGGCCCGTGGGGCTGGCCCT
GCACCGCCGAGCTTCCCGGATGAGGGCCCCCGTGTGGTACCCCGG
CGCGCCCCAGGTCGCTGAGGGACCCCGGCCAGGCGCGGAGATGGG
GTGCACGAATGTCTGCCTGGCTGTGGCTTCTCCTGTCCCTGCTGTG
CTCCCTCTGGGCCTCCAGTCCTGGGCGCCCCACCACGCCTCATCTGT
GACAGCCGAGTCTGGAGAGGTACCTCTTGGAGGCCAAGGAGGCCG
AGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAAT
ATCACTGTCCCAGACACCAAAGTTAATTCTATGCCTGGAAGAGGAT
GGAGGTCGGGCAGCAGGCCGTAGAAGTCTGGCAGGGCCTGGCCCTG
CTGTGCGAAGCTGTCTGCGGGGCCAGGCCCTGTTGGTCAACTCTTCC
CAGCCGTGGGAGCCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGTGG
CCTTCGCAGCCTCACCACTCTGCTTCGGGCTCTGCGAGCCGAGAAGG
AAGCCATCTCCCTCCAGATGCGGCCTCAGCTGCTCCACTCCGAACA
ATCACTGCTGACACTTTCGCAAACTCTTCCGAGTCTACTCCAATTTC
CTCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTGCAGGACAG
GGGACAGATGACCAGGTGTGTCCACCTGGGCATATCCACCACCTCCC
TCACCAACATTGCTTGTGCCACACCCTCCCCCGCCACTCCTGAACCCC
GTCGAGGGGCTCTCAGCTCAGCGCCAGCCTGTCCCATGGACACTCCA
GTGCCAGCAATGACATCTCAGGGGCCAGAGGAACTGTCCAGAGAGC
AACTCTGAGATCTAAGGATGTACAGGGCCAACCTTGAGGGGCCAGAG
CAGGAAGCATTGAGAGAGCAGCTTTAAACTCAGGGACAGAGCCATG
CTGGGAAGACGCCTGAGCTCACTCGGCACCCTGCAAAATTTGATGCC
AGGACACGCTTTGGAGGCGATTTACCTGTTTTGACCTACCATCAGG
GACAGGATGACCTGGAGAACTTAGGTGGCAAGCTGTGACTTCTCCAG
GTCTACGGGCATGGGCACTCCCTTGGTGGCAAGAGCCCCCTTGACA
CCGGGGTGGTGGGAACCATGAAGACAGGATGGGGGCTGGCCCTCTGG
CTCTCATGGGGTCCAAGTTTTGTGTATTCTTCAACCTCATTGACAAGA
ACTGAAACCACCAAAAAAAAAAAAAA

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FIG. 64B

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu Leu Ser
Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu Ile Cys Asp Ser
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val
Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu
Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu Ala Ile
Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe
Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr
Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg

FIG. 65

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala
Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn
Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg
Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val
Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly
Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr
Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly
Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp

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FIG. 66A

ATGTGGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCAT
CTCTGCACCCGCCCGCTCGCCAGCCCCAGCACGCAGCCCTGGGAGC
ATGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGA
GACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAGAAAAT
GTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCTGGAGCTGT
ACAAGCAGGGCCTGCGGGGCAGCCTACCAAGCTCAAGGGCCCTTG
ACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGA
AACTTCCTGTGCAACCCAGATTATCACCTTTGAAAAGTTCAAAGAGA
ACCTGAAGGACTTTCTGCTGTTCATCCCCTTTGACTGCTGGGAGCCAG
TCCAGGAGTGA

FIG. 66B

Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile Ser Ala Pro
Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val Asn Ala Ile Gln Glu
Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr
Val Glu Val Ile Ser Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg
Leu Glu Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro
Leu Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp Phe Leu
Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu

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FIG. 67A

ATGAAATATACAAGTTATATCTTGGCTTTTCAGCTCTGCATCGTTTTG
GGTTCTCTTGGCTGTTACTGCCAGGACCCATATGTAAAAGAAGCAGA
AAACCTTAAGAAATATTTTAATGCAGGTCATTAGATGTAGCGGATA
ATGGAACTCTTTTCTTAGGCATTTTGAAGAATTGGAAAAGAGGAGAGT
GACAGAAAAATAATGCAGAGCCAAATTGTCTCCTTTTACTTCAAACCT
TTTTAAAAAATTAAAGATGACCAGAGCATCCAAAAGAGTGTGGAGA
CCATCAAGGAAGACATGAATGTCAAGTTTTTCAATAGCAACAAAAAG
AAACGAGATGACTTCGAAAAGCTGACTAATTATTTCGGTAACTGACTT
GAATGTCCAACGCAAAGCAATACATGAACTCATCCAAGTGATGGCTG
AACTGTCGCCAGCAGCTAAACAGGGAAGCGAAAAAGGAGTCAGAT
GCTGTTTCGAGGTCTGAAGAGCATCCCAAGTAA

FIG. 67B

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu Gly Ser Leu
Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr
Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile
Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser
Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val
Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys
Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln
Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys
Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Arg Ala Ser Gln

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FIG. 68A

CTGGGACAGTGAATCGACAATGCCGTCTTCTGTCTCGTGGGGCATCCT
CCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGGA
TCCCCAGGGAGATGCTGCCAGAAGACAGATACATCCCACCATGATC
AGGATCACCCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTC
GCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCAACAA
TATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTC
CCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTGA
ATTTCAACCTCACGGAGATTCGGGAGGCTCAGATCCATGAAGGCTTC
CAGGAACCTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCT
GACCACCGGCAATGGCCTGTTCTCAGCGAGGGCCTGAAGCTAGTGG
ATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAGCCTTC
ACTGTCAACTTCGGGGACACCGAAGAGGGCCAAAGAAACAGATCAACG
ATTACGTGGAGAAGGGTACTCAAGGGAAAATTGTGGATTTGGTCAAG
GAGCTTGACAGAGACACAGTTTTTGCTCTGGTGAATTACATCTTCTTT
AAAGGCCAAATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGAAG
AGGACTTCCACGTGGACCAGGTGACCACCGTGAAGGTGCCTATGATG
AAGCGTTTAGGCATGTTTAACATCCAGCACTGAAGAAGCTGTCCAG
CTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCT
TCCTGCCTGATGAGGGGAACTACAGCACCTGGAAAATGAAGTCAAC
CACGATATCATCACCAAGTTCTTGAAAAATGAAGACAGAAGGTCTGC
CAGCTTACATTTACCCAACTGTCCATTACTGGAACCTATGATCTGAA
GAGCGTCTGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGG
CTGACCTCTCCGGGGTACAGAGGAGGCACCCCTGAAGCTCTCCAAG
GCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAGGGACTGAAGC
TGCTGGGGCCATGTTTTAGAGGCCATACCCATGTCTATCCCCCCGA
GGTCAAGTTCAACAAACCTTTGTCTTCTTAATGATTGAACAAAATAC
CAAGTCTCCCTCTTTCATGGGAAAAGTGGTGAATCCACCCAAAAAT
AACTGCCTCTCGCTCCTCAACCCCTCCCCTCCATCCCTGGCCCCCTCC
CTGGATGACATTAAAGAAGGGTTGAGCTGG

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FIG. 68B

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser
His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu Phe
Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe
Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp
Thr His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala
Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln
Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu Val
Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala Phe Thr Val
Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys
Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val
Phe Ala LeuVal Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val
Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser
Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro
Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile Thr Lys
Phe Leu Glu Asn Glu AspArg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile
Thr Gly Thr Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys
Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala
Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys Pro
Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val
Val Asn Pro Thr Gln Lys

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FIG. 69A-1

GCTAACCTAGTGCCTATAGCTAAGGCAGGTACCTGCATCCTTGTTTTT
GTTTAGTGGAATCCTCTATCCTTCAGAGACTCTGGAACCCCTGTGGTCT
TCTCTTCATCTAATGACCCTGAGGGGATGGAGTTTTCAGTCCCTTCCA
GAGAGGAATGTCCCAAGCCTTTGAGTAGGGTAAGCATCATGGCTGGC
AGCCTCACAGGTTTGCTTCTACTTCAGGCAGTGTCTGGGCATCAGGT
GCCCGCCCTGCATCCCTAAAAGCTTCGGCTACAGCTCGGTGGTGTGT
GTCTGCAATGCCACATACTGTGACTCCTTTGACCCCCGACCTTTCTC
GCCCTTGGTACCTTCAGCCGCTATGAGAGTACACGCAGTGGGCGACG
GATGGAGCTGAGTATGGGGCCCATCCAGGCTAATCACACGGGCACAG
GCCTGCTACTGACCTTCAGCCAGACAGAAAGTTCCAGAAAGTGAAG
GGATTGGAGGGGCCATGACAGATGCTGCTGCTCTCAACATCCTTGCC
CTGTCAACCCCTGCCAAAATTGCTACTTAAATCGTACTTCTCTGAA
GAAGGAATCGGATATAACATCATCCGGGTACCCATGGCCAGCTGTGA
CTTCTCCATCCGCACCTACACCTATGCAGACACCCCTGATGATTCCA
GTTGCACAACTTCAGCTCCAGAGGAAGATACCAAGCTCAAGATAC
CCCTGATTACCCGAGCCCTGCAGTTGGCCAGCTCCCGTTTCACTCC
TTGCCAGCCCTGGACATCACCCACTTGGCTCAAGACCAATGGAGCG
GTGAATGGGAAGGGGTCACTCAAGGGACAGCCCGGAGACATCTACC
ACCAGACCTGGGCCAGATACTTTGTGAAGTTTCTGGATGCCTATGCTG
AGCACAAAGTTACAGTTCTGGGCAGTGACAGCTGAAAATGAGCCTTCT
TGTGGGCTGTTGAGTGGATACCCCTTCCAGTGCCTGGGCTTACCCCT
GAACATCAGCGAGACTTCATTGCCCGTGACCTAGGTCTTACCCTCGCC
AACAGTACTCACCACAATGTCCGCTACTCATGCTGGATGACCAACGG
TTGCTGCTGCCCCACTGGGCAAAGGTGGTACTGACAGACCCAGAAGC
AGCTAAATATGTTTCATGGCATTGCTGTACATTGGTACCTGGACTTTCT
GGCTCCAGCCAAAGCCACCCTAGGGGAGACACACCGCTGTTCCCCA
ACACCATGCTCTTTGCTCAGAGGCCCTGTGTGGGCTCCAAGTTCTGGG
AGCAGAGTGTGCGGCTAGGCTCCTGGGATCGAGGATGACAGTACAGC
CACAGCATCATCACGAACCTCCTGTACCATGTGGTGGCTGGACCGAC
TGGAACCTTGCCCTGAACCCGAAGGAGGACCAATTGGGTGCGTAA
CTTTGTGACAGTCCCATCATTGTAGACATACCAAGGACAGTTTTA
CAACAGCCCATGTTCTACCACCTTGGCCACTTCAGCAAGTTCATTCC
TGAGGGCTCCCAAGAGAGTGGGGCTGGTTGCCAGTCAGAAGAACGACC
TGGACGCAGTGGCACTGATGCATCCCGATGGCTCTGCTGTTGTGGTGC
TGCTAAACCGCTCCTCTAAGGATGTGCCTCTTACCATCAAGGATCCTG
CTGTGGGCTTCTGTGGAGACAATCTCACCTGGCTACTCCATTACACCT
ACCTGTGGCATCGCCAGTGATGGAGCAGATACTCAAGGAGGCACTGG
GCTCAGCCTGGGCATTAAAGGGACAGAGTCAGCTCACACGCTGTCTG
TGACTAAAGAGGGCACAGCAGGGCCAGTGTGAGCTTACAGCGACGT

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FIG. 69A-2

AAGCCCCAGGGGCAATGGTTTGGGTGACTCACTTCCCCCTCTAGGTGGT
 GCCCAGGGCTGGAGGCCCTAGAAAAAGATCAGTAAGCCCCAGTGTG
 CCCCCAGCCCCATGCTTATGTGAACATGCGCTGTGTGCTGCTTGCTT
 TGGAAACT

FIG. 69B

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser Arg Val Ser
 Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln Ala Val Ser Trp Ala Ser
 Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys Val Cys
 Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr
 Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly
 Pro Ile Gln Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
 Lys Phe Gln Lys Val Lys Gly Phe Gly Ala Met Thr Asp Ala Ala Leu
 Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser
 Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe Ser
 Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser
 Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu
 Ala Gln Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys
 Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile
 Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu
 His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu
 Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln Arg Asp
 Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg
 Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val
 Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu
 Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro
 Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser
 Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn
 Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu
 Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr
 Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu
 Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn
 Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu
 Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln

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FIG. 70A

ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGG
AGCAGTCTTCGTTTCGCCAGCCAGGAAATCCATGCCCGATTTCAGAA
GAGGAGCCAGATCTTACCAAGTGATCTGCAGAGATGAAAAACGCA
GATGATATACCAGCAACATCAGTCATGGCTGCGCCCTGTGCTCAGAA
GCAACCGGGTGGAAATATTGCTGGTGCAACAGTGGCAGGGCACAGTGC
CACTCAGTGCCTGTCAAAAAGTTGCAGCGAGCCAAGGTGTTTCAACGG
GGGCACCTGCCAGCAGGCCCTGTACTTCTCAGATTTCGTGTGCCAGTG
CCCCGAAGGATTTGCTGGGAAGTGCTGTGAAATAGATACCAAGGCCA
CGTGCTACGAGGACCAGGGCATCAGCTACAGGGGCACGTGGAGCAC
AGCGGAGAGTGGCGCCGAGTGCAACCACTGGAACAGCAGCGCGTTG
GCCCAGAAGCCCTACAGCGGGCGGAGGCCAGACGCCATCAGGCTGG
GCCTGGGGAAACCACAATACTACTGCAGAAACCCAGATCGAGACTCAA
GCCCTGGTGCTACGTCTTTAAGGCGGGGAAGTACAGTCAAGATTCT
GCAGCACCCCTGCCTGTCTGAGGGAAACAGTGACTGCTACTTTGGG
AATGGGTCAGCCTACCGTGGCACGCACAGCCTCACCGAGTCGGGTGC
CTCCTGCCTCCCGTGGAAATTCATGATCCTGATAGGCAAGGTTTACAC
AGCACAGAACCCAGTGCCACGGCACTGGGCCTGGGCAAAACATAATT
ACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTG
AAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTC
CACCTGCGGCCTGAGACAGTACAGCCAGCCTCAGTTTCGCATCAAAG
GAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCT
TTGCCAAGCACAGGAGGTGCGCGGGAGAGCGGTTCTGTGCGGGGGC
ATACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAG
GAGAGGTTTCCGCCCCACCACTGACGGTGATCTTGGGCAGAACATA
CCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCAGATAATT
TACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACAT
TGCGCTGTGTCAGCTGAAAACGGATTTCGTCCCGCTGTGCCAGGAGA
GCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGGGGACCTGCAGCTG
CCGGACTGGACGGAGTGTGAGCTTCCGGCTACGGCAAGCATGAGGC
CTTGTCTCCTTTCTATTCCGAGCGGCTGAAGGAGGCTCATGTACAGCT
GTACCCATCCAGCCGCTGCACATCAACAATTACTTAACAGAACAG
TCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGGCGGGCC
CAGGCAAACTTGACGACGCCTGCCAGGGCGATTTCGGAGAGGCCCCCT
GGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGCT
GGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACCAAG
GTTACCAACTACCTAGACTGGATTTCGTGACAACATGCGACCGTGACC
AGGAACACCCGACTCCTCAAAAGCAAAATGAGATCC

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FIG. 70B

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly Ala Val
Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg Gly Ala Arg Ser Tyr
Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln Gln His Gln Ser Trp
Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly
Arg Ala Gln Cys His Ser Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn
Gly Gly Thr Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro
Glu Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu
Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu Cys
Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly Arg Arg Pro Asp
Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys Arg Asn Pro Asp Arg Asp
Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser
Thr Pro Ala Cys Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr
Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met
Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu Gly Leu
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys Pro Trp Cys His
Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser
Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe
Ala Asp Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser
Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser
Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile Leu Gly
Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe Glu Val Glu Lys
Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu
Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg
Thr Val Cys Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu
Leu Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Pro
Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly
Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg
Asp Asn Met Arg Pro

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FIG. 71A

ATCACTCTCTTTAATCACTACTCACATTAACCTCAACTCCTGCCACAA
 TGTACAGGATGCAACTCCTGTCTTGCAITGCACTAATTCTTGCACTTG
 TCACAAACAGTGCACCTACTTCAAGTTCGACAAAGAAAAACAAAGAAA
 ACACAGCTACAACCTGGAGCATTCTACTGCTGGATTACAGATGATTTTG
 AATGGAATTAATAATTACAAGAATCCCAAACTCACCAGGATGCTCAC
 ATTTAAGTTTTACATGCCCCAAGAAGGCCACAGAACTGAAACAGCTTC
 AGTGTCTAGAAGAAGAACTCAAACCTCTGGAGGAAGTGCTGAATTTA
 GCTCAAAGCAAAAACTTTCACTTAAGACCCAGGGACTTAATCAGCAA
 TATCAACGTAATAGTTCTGGAACATAAAGGGATCTGAAACAACATTCA
 TGTGTGAATATGCAGATGAGACAGCAACCATTGTAGAATTTCTGAAC
 AGATGGATTACCTTTTGTCAAAGCATCATCTCAACACTAACTTGATAA
 TTAAGTGCTTCCCACTTAAAAACATATCAGGCCCTTCTATTTATTTATTTA
 AATATTTAAATTTTATATTTATTGTTGAATGTATGGTTGCTACCTATTG
 TAACTATTATTCTTAATCTTAAAACTATAAATATGGATCTTTTATGAT
 TCTTTTTGTAAGCCCTAGGGGCTCTAAAATGGTTACCTTATTTATCC
 CAAAAATATTTATTATTATGTTGAATGTTAAATATAGTATCTATGTAG
 ATTGGTTAGTAAAACTATTTAATAAATTTGATAAATATAAAAAAAAAA
 AAACAAAAAAAAAAAA

FIG. 71B

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu Val Thr Asn
 Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Lys Lys Thr Gln Leu Gln Leu Glu
 His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
 Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr
 Glu Leu Lys Gln Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
 Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser
 Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
 Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys
 Gln Ser Ile Ile Ser Thr Leu Thr

FIG. 72A-1

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ATGCAAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTTTTGGCATTCT
GCTTTAGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAACCTGTCA
TGGGACTATATGCAAAAGTGATCTCGGTGAGCTGCCTGTGGACGCAAG
ATTTCTCCTAGAGTGCCAAAATCTTTTCCATTCAACACCTCAGTCGT
GTACAAAAAGACTCTGTTGTAGAAATTCACGGATCACCTTTTCAACAT
CGCTAAGCCAAGGCCACCTGGATGGGTCTGCTAGGTCTACCATCC
AGGCTGAGGTTTATGTATACAGTGGTCAATTACATTAAGAAACATGGCT
TCCCATCCTGTCACTCTTCATGCTGTTGGTGTATCCTACTGGAAGCT
TCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAAG
AAGATGATAAAGTCTTCCCTGGTGGGAAGCCATACATATGTCTGGCAG
GTCCTGAAAGAGAATGGTCCAATGGCTCTGACCACCTGTGCCTTAC
CTACTCATATCTTTCTCATGTGGACCTGGTAAAAAGACTTGAATTCAGG
CCTCATTTGGAGCCCTACTAGTATGTAGAGAAGGGAGTCTGGCCAAAG
AAAAGACACAGACCTTGCACAAAATTTATACTACTTTTGTGTTATTG
ATGAAGGGAAAAGTTGGCACTCAGAAACAAAGAACTCTTGATGCA
GGATAGGGATGCTGCATCTGCTCGGGCCTGGCCTAAAATGCACACAG
TCAATGGTTATGTAAACAGGTCTCTGCCAGGTCTGATTGGATGCCACA
GGAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACTCTGAA
GTGCACTCAATATTCTCGAAGGTACACATTTCTGTGAGGAACCAT
CGCCAGGCGTCTTGGAAATCTCGCCAATAACTTTCTTACTGTCTCAA
ACACTCTGTATGGACCTTGGACAGTTTCTACTGTTTGTGCATATCTCTT
CCCACCAACATGATGGCATGGAAGCTTATGTCAAAGTAGACAGCTGT
CCAGAGGAACCCCAACTACGAATGAAAAATAATGAAGAAGCGGAAG
ACTATGATGATGATCTTACTGATTCTGAAATGGATGTGGTCAGGTTTG
ATGATGACAACTCTCCTTCTTATCCAAATTCGCTCAGTTGCCAAGA
AGCATCTCTAAAATCTGGGTACATTACATTGCTGCTGAAGAGGAGGAC
TGGGACTATGCTCCCTTAGTCTCGCCCCGATGACAAAGTTATAAA
AGTCAATATTTGAACAATGGCCCTCAGCGGATTGGTAGGAAGTACAA
AAAAGTCCGATTATGGCATAACAGATGAAACCTTTAAGACTCTGTG
AAGCTATTACAGCATGAATCAGGAATCTTGGGACCTTTACTTTATGGGG
AAGTTGGAGACACACTGTTGATTATATTTAAGAAATCAAGCAAGCAGA
CCATATAACATCTACCCTCACGGAATCACTGATGTCCGTCCTTTGTAT
TCAAGGAGATTACCAAAAGGTGTAAAAACATTTGAAGGATTTTCCAAT
TCTGCCAGGAGAAAATTTCAAATATAAATGGACAGTACTGTAGAGAAG
ATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTA
GTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC
TCCTCATCTGCTACAAAGAATCTGTAGATCAAAGAGGAACCAGATA
ATGTCAGACAAAGAGGAATGTCATCCTGTTTCTGTATTGTGATGAGA
CGAAGCTGGTACCTCACAGAGAATATACAACGCTTCTCCCCAATCCA
GCTGGAGTGCAGCTTGAGGATCCAGAGTTCCAAGCCTCCAACATCAT
GCACAGCATCAATGGCTATGTTTGTAGTGTGAGTTGTGAGTTGTG
TTTGCATGAGGTGGCATACTGGTACATTCTAAGCATTTGGAGCAGAGA
CTGACTTCTCTTCTGTCTTCTCTGGATATACCTTCAAACACAAAAT

FIG. 72A-2 299/497

GGTCTATGAAGACACACTCACCCCTATTCCCATTTCTCAGGAGAACTGT
CTTCATGTGTCGATGGAAAAACCCAGGTCTATGGATTCTGGGGTGCCACA
ACTCAGACTTTTCGGAACAGAGGCATGACCGCCTTACTGAAGGTTTTCT
AGTTGTGACAAGAACACTGGTGATTATTACGAGGACAGTTATGAAGA
TATTTCAGCATACTTGCTGAGTAAAAACAATGCCATTGAACCAAGAA
GCTTCTCCCAGAATTCAAGACACCGTAGCACTAGGCCAAAAGCAATTT
AATGCCACCACAATTCCAGAAAAATGACATAGAGAAGACTGACCCTTG
GTTTGCACACAGAACACCTATGCCTAAAATACAAAATGTCTCCTCTA
GTGATTGTGTGATGCTCTTGCGACAGAGTCCCTACTCCACATGGGCTAT
CCTTATCTGATCTCCAAGAAGCCAAAATATGAGACTTTTCTGATGATC
CATCACCTGGAGCAATAGACAGTAATAACAGCCTGTCTGAAATGACA
CACTTCAGGCCACAGCTCCATCACAGTGGGGACATGGTATTTACCCC
TGAGTCAGGCCTCCAATTAAGATTAAATGAGAAAATGGGGACAACCTG
CAGCAACAGAGTTGAAGAACTTGATTTCAAAGTTTCTTAAGTATGATC
AATAATCTGATTTCAACAATTCCATCAGACAATTTGGCAGCAGGTACT
GATAATACAAGTTTCTTAGGACCCCCAAGTATGCCAGTTCATTATGAT
AGTCAATTAGATACCACTCTATTTGGCAAAAAAGTCATCTCCCCTTACT
GAGTCTGGTGGACCTCTGAGCTTGAGTGAAGAAAATATCTGATCAAA
GTTGTTAGAAATCAGGTTTAATGAATAGCCAAAGAAAGTTCATGGGGAA
AAAATGTATCGTCAACAGAGAGTGGTAGGTTATTTAAAGGGAAAAGA
GCTCATGGACCTGCTTTGTTGACTAAAGATAATGCCTTATTCAAAGT
AGCATCTCTTTGTTAAAGACAAAACAAAACCTTCCAATAATTGAGCAACT
AATAGAAAGACTCACATTGATGGCCCATCATTATTAATTGAGAATAG
TCCATCAGTCTGGCAAAATATATTAGAAAAGTGACACTGAGTTAAAAA
AAGTGACACCTTTGATTCATGACAGAATGCTTATGGACAAAAATGCT
ACAGCTTTGAGGCTAAATCATATGTCAAATAAACTACTTCATCAAA
AAACATGGAAATGGTCCAACAGAAAAAAGAGGGCCCCATTCCACCA
GATGCACAAAATCCAGATATGTCGTTCTTTAAGATGCTATTTCTGCCA
GAATCAGCAAGGTGGATACAAAGGACTCATGGAAAGAACTCTCTGAA
CTCTGGGCAAGGCCCCAGTCCAAAGCAATTAGTATCCTTAGGACCGAG
AAAAATCTGTGGAAAGGTCAGAAATTTCTTGCTGAGAAAAACAAAGTG
GTAGTAGGAAAGGGTGAATTTACAAAGGACGTAGGACTCAAAGAGA
TGGTTTTTCCAAGCAGCAGAAACCTATTCTTACTAACTTGGATAATT
TACATGAAAATAATACACACAATCAAGAAAAAAAATTCAGGAAGA
AATAGAAAAGAAAGGAAACATTAATCCAAGAGAAATGTAGTTTTGCCTC
AGATACATACAGTGACTGGCACTAAGAATTTTCATGAAGAACCTTTTC
TTACTGAGCACTAGGCAAAATGTAGAAGGTTTCATATGACGGGGCATA
TGCTCCAGTACTTCAAGATTTTAGGTCATTAAATGATTCAACAAATAG
AACAAAAGAAAACACAGCTCATTTCTCAAAAAAAGGGGAGGAAGAA
AACTTGGAAGGCTTGGGAAATCAAACCAGCAAAATGTAGAGAAATAT
GCATGCACCACAAGGAATATCTCCTAATACAAGCCAGCAGAAATTTTG
TCACGCAACGTAGTAAGAGAGCTTTGAAACAATTCAGACTCCCACTA

FIG. 72A-3

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GAAGAAACAGAACTTGAAGGATAATTGTGGATGACACCTCAAC
CCAGTGGTCCAAAAACATGAAACATTTGACCCCGAGCACCCCTCACAC
AGATAGACTACAATGAGAAGGAGAAAGGGGCCATTACTCAGTCTCCC
TTATCAGATTGCCTTACGAGGAGTCATAGCATCCCTCAAGCAAATAGA
TCTCCATTACCCATTGCAAAGGTATCATCATTTCCATCTATTAGACCTA
TATATCTGACCAGGGTCTATTCCAAGACAACCTCTCTCATCTTCCAG
CAGCATCTTTATAGAAAAGAAAGATTCTGGGGTCCAAGAAAGCAGTCAT
TTCTTACAAGGAGCCAAAAAAATAACCTTTCTTTAGCCATTCTAACCC
TTGGAGATGACTGGTGATCAAAGAGAGGTTGGCTCCCTGGGGACAAG
TGCCACAAATTCAGTCACATACAAGAAAGTTGAGAACTGTCTCTCCC
GAAACCAAGACTTGCCCAAAACATCTGGCAAAGTTGAATTGCTTCCAA
AAGTTCACATTTATCAGAAGGACCTATTCCCTACGGAAACTAGCAATG
GGTCTCCTGGCCATCTGGATCTCGTGGAAGGGAGCCTTCTTCAGGGAA
CAGAGGGAGCGATTAAAGTGAATGAAGCAAACAGACCTGGAAAGAGT
TCCCTTTCTGAGAGTAGCAACAGAAAGCTCTGCAAAGACTCCCTCCAA
GCTATTGGATCCTCTTGCTTGGGATAACCACTATGGTACTCAGATACC
AAAAGAAGAGTGGAAATCCCAAGAGAAGTCACCAAGAAAAACAGCT
TTTAAGAAAAAGGATACCATTTTGTCCCTGAACGCTTGTGAAGCAAT
CATGCAATAGCAACAATAAATGAGGGACAAAATAAGCCCGAAATAG
AAGTCACCTGGGCAAAGCAAGGTAGGACTGAAAGGCTGTGCTCTCAA
AACCCACCAAGTCTTGAAACGCCATCAACGGGAAATAACTCGTACTAC
TCTTCAGTCAGATCAAGAGGAAATTGACTATGATGATACCAATCAGT
TGAAATGAAGAAGGAAGATTTTGACATTTATGATGAGGATGAAAAATC
AGAGCCCCCGCAGCTTTCAAAGAAAACACGACACTATTTTATTGCTG
CAGTGGAGAGGCTCTGGGATTATGGGATGAGTAGCTCCCCACATGTT
CTAAGAAACAGGGCTCAGAGTGGCAGTGTCCCTCAGGTTCAAGAAAGT
TGTTTTCCAGGAATTTACTGATGGCTCCTTTACTCAGCCCTTATACCGT
GGAGAATAAATGAACATTTGGGACTCCTGGGGCCATATATAAGAGC
AGAAGTTGAAGATAATATCATGGTAACCTTCAGAAATCAGGCCTCTC
GTCCCTATTCTCTATTCTAGCCTTATTTCTTATGAGGAAGATCAGAG
GCAAGGAGCAGAACCTAGAAAAAATTTGTCAAGCCTAATGAAACCA
AAACTTACTTTTGGAAAGTGCAACATCATATGGCACCCACTAAAGAT
GAGTTTGAAGTCAAAGCCTGGGCTTATTTCTCTGATGTTGACCTGGAA
AAAGATGTGCACTCAGGCCTGATTGGACCCCTCTCGTGTCTGCCACACT
AACACACTGAACCCCTGCTCATGGGAGACAAGTGACAGTACAGGAATT
TGCTCTGTTTTTACCATCTTTGATGAGACCAAAAGCTGGTACTTCACT
GAAAAATAGGAAAGAACTGCAGGGCTCCCTGCAATATCCAGATGGA
AGATCCCACCTTTTAAAGAGAAATTATCGCTTCCATGCAATCAATGGCTA
CATAATGGATACACTACCTGGCTTAGTAATGGCTCAGGATCAAAGGA
TTGATGGTATCTGCTCAGCATGGGCAGCAATGAAAAACATCCATTCT
ATTCATTTCAAGTGGACATGTGTTCACTGTACGAAAAAAGAGGAGTA
TAAATGGCACTGTACAATCTCTATCCAGGTGTTTTTGAGACAGTGGAA

FIG. 72A-4

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AATGTTACCATCCAAAGCTGGAATTTGGCGGGTGAATGCCTTATTGG
CGAGCATCTACATGCTGGGATGAGCACACTTTTTCTGGTGTACAGCAA
TAAGTGTCCAGACTCCCCTGGGAATGGCTTCTGGACACATTAGAGATTT
TCAGATTACAGCTTCAGGACAATATGGACAGTGGGCCCCAAAGCTGG
CCAGACTTCATTATTCGGATCAATCAATGCCTGGAGCACCAGGAG
CCCTTTTCTTGGATCAAGGTGGATCTGTTGGCACCAATGATTATTCAC
GGCATCAAGACCGAGGGTGCCCGTCAGAAGTTCTCCAGCCTTACAT
CTCTCAGTTTATCATCATGTATAGTCTTGATGGGAAGAAGTGGCAGA
CTTATCGAGGAAATTCCACTGGAACCTTAATGGTCTTCTTTGGCAATG
TGGATTACATCTGGGATAAAACACAATATTTTAAACCTCCAATTATTG
TTCGATACATCCGTTTGCAACCAACTCATTATAGCATCTCGCAGCACTC
TTCGCATGGAGTTGATGGGCTGTGATTTAAATAGTTGCAGCATGCCAT
TGGGAATGGAGAGTAAAGCAATATCAGATGCACAGATTACTGCTTCA
TCTACTTTACCAATATGTTTGCCACCTGGTCTCCTTCAAAGCTCGA
CTTCACCTCCAACCGAGGAGTAATGCCTGGAGACCTCAGGTGAATAA
TCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGTCA
CAGGAGTAACTACTCAGGGAGTAAATCTCTGCTTACCAGCATGTAT
GTGAAGGAGTTCCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGAC
TCTCTTTTTCAGAAATGGCAAAGTAAAGGTTTTCAGGGAAATCAAGA
CTCCTTACACCTGTGGTGAACCTCTCTAGACCCACCGTTACTGACTCG
CTACCTTCGAATTCACCCCGAGATTGGGTGCACCAGATTGCCCTGAG
GATGGAGGTTCTGGGCTGCGAGGCACAGGACCTCTACTGAGGGTGGC
CACTGCAGCACCTGCCACTGCCGTACCTCTCCCTCAGCTCCAGG
GCAGTGTCCCTCCCTGGCTTGCTTCTACCTTTGTGCTAAATCCTAGC
AGACACTGCCTTGAAGCCTCCTGAATTAACATCATCAGTCCTGCATT
TCTTTGGTGGGGGGCCAGGAGGGTGCATCCAATTTAACTTAACTTTA
CCTATTTTCTGCAGCTGCTCCAGATTACTCCTTCCATCCAATATACT
AGGCAAAAAGAAGTGAGGAGAAACCTGCATGAAAGCATTCTTCCCTG
AAAAGTTAGGCCTCTCAGAGTCAACCACTTCTCTGTTGTAGAAAACT
ATGTGATGAAACTTTGAAAAAGATATTTATGATGTTAAACATTTAGGT
TAAGCTCATACTGTTTAAAAATAAACTCTCAGTTGTTTATTATCTGGA
TCAAGCATGGAACAAAGCATGTTTCAGGATCAGATCAATACAATCTT
GGAGTCAAAAAGGCAAATCATTTGGACAATCTGCAAAATGGAGAGAA
TACAATACTACTACAGTAAAGTCTGTTTCTGCTTCCCTTACACATAGA
TATAATTATGTTATTATTAGTCATTATGAGGGGCACACTCTTATCTCCAA
AACTAGCATTCTTAACTGAGAATTATAGATGGGGTTCAAGAATCCC
TAAGTCCCCTGAAATTATATAAGGCATTCTGTATAAATGCAATGTGC
ATTTTTCTGACGAGTGTCCATAGATATAAAGCCATTTGGTCTTAATCTT
GACCAATAAAAAATAAGTCAGGAGATGCAATTGTTGAAAGCTTTG
AAATAAAAAATAACAATGTCTTCTTGAATTTGTGATGGCCAAGAAAGA
AAATGATGA

FIG. 72B-1

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe Cys Phe Ser
Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr Met Gln Ser
Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe
Pro Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His
Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile
Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro
Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr
Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly
Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro
Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn
Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys
Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser
Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg
Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu
Ile Gly Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro
Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln
Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp
Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met Glu
Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn
Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val
Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys
Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr
Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro
Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser
Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg
Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile
Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg
Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala Ser
Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn
Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg
Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln
Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys
His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val
Phe Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe

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FIG. 72B-2

Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr
 Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn
 Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg Ser Thr Arg Gln
 Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys Thr Asp Pro Trp
 Phe Ala His Arg Thr Pro Met Pro Lys Ile Gln Asn Val Ser Ser Ser Asp Leu Leu
 Met Leu Leu Arg Gln Ser Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu
 Ala Lys Tyr Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
 Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val
 Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly Thr Thr
 Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser Thr Ser Asn Asn Leu
 Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu
 Gly Pro Pro Ser Met Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly
 Lys Lys Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn
 Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp Gly
 Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys Arg Ala His Gly
 Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys Val Ser Ile Ser Leu Leu
 Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp
 Gly Pro Ser Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser
 Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp
 Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr Ser Ser
 Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala
 Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg
 Trp Ile Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro Ser Pro
 Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu Gly Gln Asn Phe Leu
 Ser Glu Lys Asn Lys Val Val Val Gly Lys Gly Glu Phe Thr Lys Asp Val Gly
 Leu Lys Glu Met Val Phe Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp
 Asn Leu His Glu Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile
 Glu Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr
 Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr Arg Gln
 Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala Pro Val Leu Gln Asp Phe Arg
 Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys His Thr Ala His Phe Ser Lys
 Lys Gly Glu Glu Glu Asn Leu Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val
 Glu Lys Tyr Ala Cys Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe
 Val Thr Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu
 Thr Glu Leu Glu Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser Lys Asn
 Met Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys Glu
 Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser Ile
 Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser Ser Phe Pro Ser Ile
 Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe Gln Asp Asn Ser Ser His Leu Pro

FIG. 72B-3

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Ala Ala Ser Tyr Arg Lys Lys Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu
 Gln Gly Ala Lys Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr
 Gly Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr
 Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr Ser
 Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys Asp Leu Phe Pro
 Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu
 Leu Gln Gly Thr Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys
 Val Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu
 Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu
 Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Lys Asp Thr Ile
 Leu Ser Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly
 Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg
 Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg
 Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu
 Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg
 Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp
 Tyr Gly Met Met Ala Gln Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val
 Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro
 Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg
 Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro
 Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu
 Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val
 Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr
 Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu
 Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln
 Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu
 Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr
 Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro
 Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly
 Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys
 Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr
 Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu
 His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr
 Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln
 Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala
 Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile
 Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser
 Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly
 Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile

FIG. 72B-4

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Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr
His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn
Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr
Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu
His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu
Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln
Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser
Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe
Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu
Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg
Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr

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FIG. 73A

TCCACCTGTCCCCGCAGCGCCGGCTCGCGCCCTCCTGCCGCAGCCACC
GAGCCGCCGTCTAGCGCCCCGACCTCGCCACCATGAGAGCCCTGCTG
GCGCGCCTGCTTCTCTGCGTCTGGTCTGTGAGCGACTCCAAAGGCAGC
AATGAACTTCATCAAGTTCCATCGAACTGTGACTGTCTAAATGGAGGA
ACATGTGTGTCCAACAAGTACTTCTCCAACATTCACTGGTGCAACTGC
CCAAAGAAATTCGGAGGGCAGCACTGTGAAATAGATAAGTCAAAAAAC
CTGCTATGAGGGGAATGGTCACTTTTACCGAGGAAAGGCCAGCACTG
ACACCATGGGCCGGCCCTGCCTGCCCTGGAACCTCGCCACTGTCTTC
AGCAAACGTACCATGCCCACAGATCTGATGCTCTTCAGCTGGGCCTGG
GGAAACATAATTACTGCAGGAACCCAGACAACCCGAGGCGACCCCTGG
TGCTATGTGCAGGTGGGCCTAAAGCCGCTTGTCGAAGAGTGCATGGT
GCATGACTGCGCAGATGGAAAAAAGCCCTCCTCTCCTCCAGAAGAAT
TAAAATTTCACTGTGGCCAAAAGACTCTGAGGCCCGCTTTAAGATTA
TTGGGGGAGAATTCACCAACCATCGAGAACCAGCCCTGGTTTGGCGCC
ATCTACAGGAGGCACCGGGGGGCTCTGTCACTACGTGTGTGGAGG
CAGCCTCATCAGCCCTTGCTGGGTGATCAGCGCCACACACTGCTTCAT
TGATTACCCAAAGAAGGAGGACTACATCGTCTACCTGGGTGCTCAA
GGCTTAACTCCAACACGCAAGGGGAGATGAAGTTTGAGGTGGAAAAAC
CTCATCCTACACAAGGACTACAGCGCTGACACGCTTGCTCACCACAAC
GACATTGCCTTGCTGAAGATCCGTTCCAAGGAGGGCAGGTGTGCGCA
GCCATCCCGGACTATACAGACCATCTGCCTGCCCTCGATGTATAACGA
TCCCCAGTTTGGCACAAGCTGTGAGATCACTGGCTTTGGAAAAAGAGA
ATTCTACCGACTATCTCTATCCGGAGCAGCTGAAGATGACTGTTGTGA
AGCTGATTTCCCAACCGGGAGTGTACAGCAGCCCCACTACTACGGCTCTG
AAGTCACCACCAAAATGCTGTGTGCTGCTGACCCACAGTGAAAAACA
GATTCTCTGCCAGGGAGACTCAGGGGGACCCCTCGTCTGTTCCCTCCAA
GGCCGCATGACTTTGACTGGAATTGTGAGCTGGGGCCGTGGATGTGC
CCTGAAGGACAAGCCAGGCGTCTACACGAGAGTCTCACACTTCTTAC
CCTGGATCCGCAGTCACACCAAGGAAGAGAATGGCCTGGCCCTCTGA
GGGTCCCCAGGGAGGAAACGGGCACCAACCCGCTTCTTGCTGGTTGTG
ATTTTGCAGTAGAGTCATCTCCATCAGCTGTAAGAAGAGACTGGGA
AGAT

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FIG. 73B

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser Asp Ser
Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn Cys Pro Lys
Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn
Gly His Phe Tyr Arg Gly Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro
Trp Asn Ser Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg
Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val His
Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys
Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr
Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys
Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys
Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg
Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro
Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys
Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr
Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp
Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val
Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser
His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu

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FIG.74A

TCCTGCACAGGCAGTGCCTTGAAGTGCTTCTTCAGAGACCTTTCTTCA
TAGACTACTTTTTTCTTTAAGCAGCAAAAGGAGAAAAATTGTCATCA
AGGATATTCCAGATTCTTGACAGCATTCTCGTCATCTCTGAGGACATC
ACCATCATCTCAGGATGAGGGGCATGAAGCTGCTGGGGGCGCTGCTG
GCACTGGCGGCCCTACTGCAGGGGGCCGTGTCCCTGAAGATCGCAGC
CTTCAACATCCAGACATTGGGGGAGACCAAGATGTCCAATGCCACCT
CGTCAGCTACATTGTGCAGATCCTGAGCCGCTATGACATCGCCCTGGT
CCAGGAGGTCAGAGACAGCCACCTGACTGCCGTGGGGAAGCTGCTGG
ACAACCTCAATCAGGATGCACCAGACACCTATCACTACGTGGTCAGT
GAGCCACTGGGACGGAACAGCTATAAGGAGCGCTACCTGTTCTGTGA
CAGGCCTGACCAGGTGTCTGCGGTGGACAGCTACTACTACGATGATG
GCTGCGAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATT
GTCAGGTTCTTCTCCCGTTACAGAGGTCAGGGAGTTTGCCATTGTT
CCCCTGCATGCGGCCCGGGGGACGCAGTAGCCGAGATCGACGCTCT
CTATGACGTCTACCTGGATGTCCAAGAGAAATGGGGCTTGGAGGACG
TCATGTTGATGGGCGACTTCAATGCGGGCTGCAGCTATGTGAGACCCT
CCCAGTGGTCATCCATCCGCTGTGGACAAGCCCCACCTTCCAGTGGC
TGATCCCCGACAGCGCTGACACCACAGCTACACCCACGCACTGTGCCT
ATGACAGGATCGTGGTTGCAAGGATGCTGCTCCGAGGCGCCGTTGTT
CCGACTCGGCTCTTCCCTTTAACTTCCAGGCTGCCTATGGCCTGAGTG
ACCAACTGGCCCAAGCCATCAGTGACCACTATCCAGTGGAGGTGATG
CTGAAGTGAGCAGCCCTCCCCACACCAAGTTGAACTGCAG

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FIG. 74B

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu Leu Gln
Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys
Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp Ile
Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu
Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro
Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln
Val Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val
Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile
Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu Asp
Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln
Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser
Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln
Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val
Glu Val Met Leu Lys

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FIG. 75A

GCTGCATCAGAAGAGGCCATCAAGCACATCACTGTCCTTCTGCCATGG
CCCTGTGGATGCGCCTCCTGCCCTGCTGGCGCTGCTGGCCCTCTGGG
GACCTGACCCAGCCGCAGCCTTTGTGAACCAACACCTGTGCGGCTCAC
ACCTGGTGGAAGCTCTCTACCTAGTGTGCGGGGAACGAGGCTTCTTCT
ACACACCCAAGACCCGCCGGAGGCAGAGGACCTGCAGGTGGGGCA
GGTGGAGCTGGGCGGGGGCCCTGGTGCAGGCAGCCTGCAGCCCTTGG
CCCTGGAGGGGTCCCTGCAGAAGCGTGGCATTGTGGAACAATGCTGT
ACCAGCATCTGCTCCCTCTACCAGCTGGAGAATACTGCAACTAGACG
CAGCCCGCAGGCAGCCCCCACC CGCCCTCCTGCACCGAGAGAGA
TGGAATAAAGCCCTTGAACCAGC

FIG. 75B

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu Trp Gly
Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val
Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr
Arg Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile
Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn

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FIG. 76A

ATGGGAGGTTGGTCTTCCAAACCTCGACAAGGCATGGGGACGAATCT
TTCTGTTCCCAATCCTCTGGGATTCTTTCCCGATCACCAGTTGGACCT
GCGTTCGGAGCCAACTCAAACAATCCAGATTGGGACTTCAACCCCAA
CAAGGATCACTGGCCAGAGGCAATCAAGGTAGGAGCGGGAGACTTC
GGGCCAGGGTTCACCCACCACACGGCGGTCTTTTGGGGTGAGCCC
TCAGGCTCAGGGCATATTGACAACAGTGCCAGCAGCGCCTCCTCTG
TTTCCACCAATCGGCAGTCAGGAAGACAGCCTACTCCCATCTCTCCAC
CTCTAAGAGACAGTCATCCTCAGGCCATGCAGTGGAACTCCACAACA
TTCCACCAAGCTCTGCTAGATCCCAGATGAGGGGCCTATATTTTCT
GCTGGTGGCTCCAGTTCGGGAACAGTAAACCTGTTCGGACTACTGTC
TCACCCATATCGTCAATCTTCTCGAGGACTGGGGACCCTGCACCGAAC
ATGGAGAGCACAAACATCAGGATTCTAGGACCCCTGCTCGTGTTACA
GGCGGGGTTTTCTTGTGTTGACAAGAATCCTCACAAATACCACAGAGTCT
AGACTCGTGGTGGACTTCTCTCAATTTTCTAGGGGGAGCACCCACGTG
TCCTGGCCAAAATTTCGAGTCCCCAACCTCCAATCACTACCAACCTC
TTGTCCTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTTT
ATCATATTCTCTTTCATCCTGCTGCTATGCCTCATCTTCTGTGTGGTTC
TTCTGGACTACCAAGGTATGTTGCCCGTTTGTCTCTACTTCCAGGAA
CATCAACTACCAGCACGGGACCATGCAAGACCTGCACGATTCTGCT
CAAGGAACCTCTATGTTTCCCTCTTGTGTGTACAAAACCTTCGGAC
GGAAACTGCACTTGTATTCCCATCCCATCATCTGGGCTTTCGCAAGA
TTCCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGCTCAGTTTACTA
GTGCCATTGTTCAGTGGTTCGACGGGCTTTCCTCCCACTGTTTGCTTT
CAGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTACAACATCT
TGAGTCCCTTTTACCTCTATTACCAATTTTCTTTTGTCTTTGGGTATAC
ATTGA

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FIG. 76B

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro
Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala Asn
Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp His Trp Pro Glu Ala Ile
Lys Val Gly Ala Gly Asp Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu
Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro
Val Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg
Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu
Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
Asn Pro Val Pro Thr Thr Val Ser Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp
Pro Ala Pro Asn Met Glu Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser
Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr
Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp
Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Ala
Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
Trp Val Tyr Ile

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FIG. 77A

CGAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTA
 CAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCCTGCTCTGCCTGC
 CCTGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCTTATCCAGGC
 CTTTGTGACAACGCTATGCTCCGCGCECATCGTCTGCACCAGCTGGCCT
 TTGACACCTACCAGGAGTTTGAAGAAGCCTATATCCCAAAGGAACAG
 AAGTATTCATTCTCTGCAGAACCCCCAGACCTCCCTCTGTTTCTCAGAG
 TCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAA
 CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTGTGGCTGGA
 GCCCGTGCAGTTCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGG
 CGCCTCTGACAGCAACGTCTATGACCTCCTAAAGGACCTAGAGGAAG
 GCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGGACT
 GGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAACTCACA
 CAACGATGACGCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAG
 GAAGGACATGGCAAGGTGCGAGACATTCTGCGCATCGTGCAGTGCCG
 CTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTG
 TGACCCCTCCCCAGTGCCTCTCTGGCCCTGGAAGTTGCCACTCCAGT
 GCCCACCAGCCTGTCTTAATAAAATTAAGTTGCATC

FIG. 77B

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu
 Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu Ser Arg Pro Phe Asp
 Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln
 Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro
 Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr
 Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
 Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala
 Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
 Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Ala Leu Leu Lys Asn Tyr Gly
 Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile
 Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe

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FIG. 78A

ATGTATTCCAATGTGATAGGAACTGTAACCTCTGGAAAAAGGAAGGT
TTATCTTTTGTCCITGCTGCTCATTGGCTTCTGGGACTGCGTGACCTGT
CACGGGAGCCCTGTGGACATCTGCACAGCCAAGCCGCGGGACATTCC
CATGAATCCCAATGTGCATTACCCTCCCCGGAGAGAAGGCAACTG
AGGATGAGGGCTCAGAACAGAAGATCCCGGAGGCCACCAACCGCG
TGTCTGGGAACTGTCCAAGGCCAATTCCCGCTTTGTACCACTTTCTA
TCAGCACCTGGCAGATTCCAAGAATGACAATGATAACATTTTCCTGTC
ACCCCTGAGTATCTCCACGGCTTTTGCTATGACCAAGCTGGGTGCCTG
TAATGACACCCCTCCAGCAACTGATGGAGGTATTAAAGTTTGACACCAT
ATCTGAGAAAACATCTGATCAGATCCACTTCTTCTTTGCCAAACTGAA
CTGCCGACTCTATCGAAAAGCCAACAAATCCTCCAAGTTAGTATCAGC
CAATCGCCTTTTGGAGACAAATCCCTTACCTTCAATGAGACCTACCA
GGACATCAGTGAGTTGGTATATGGAGCCAAGCTCCAGCCCCTGGACT
TCAAGGAAAATGCAGAGCAATCCAGAGCGGCCATCAACAAATGGGTG
TCCAATAAGACCGAAGGCCGAATCACCGATGTCATTCCCTCGGAAGC
CATCAATGAGCTCACTGTTCTGGTGCTGGTTAACACCATTACTTCAA
GGGCCTGTGGAAGTCAAAGTTTCAGCCCTGAGAACACAAGGAAGGAAC
TGTTCTACAAAGCTGATGGAGAGTCGTGTTGAGCATCTATGATGTACC
AGGAAGGCAAGTTCGGTTATCGGCGCGTGGCTGAAGGACCCAGGTG
CTTGAGTTGCCCTTCAAAGGTGATGACATCACCATGGTCTCATCTTG
CCCAAGCCTGAGAAGAGCCTGGCCAAGGTGGAGAAGGAACCTACCCC
AGAGGTGCTGCAGGAGTGGCTGGATGAATTGGAGGAGATGATGCTGG
TGGTCCACATGCCCCGCTTCCGCATTGAGGACGGCTTCAGTTGAAGG
AGCAGCTGCAAGACATGGGCCTTGTCGATCTGTTGAGCCCTGAAAAG
TCCAAACTCCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTC
TCAGATGCATTCCATAAGGCAITTTCTTGAGGTAAATGAAGAAGGCAG
TGAAGCAGCTGCAAGTACCGCTGTTGTGATTGCTGGCCGTTCCGCTAAA
CCCCAACAGGGTGACTTTCAAGGCCAACAGGCCTTTCCTGGTTTTTAT
AAGAGAAAGTTCTCTGAACACTATTATCTTCATGGGCAGAGTAGCCA
ACCTTGTGTTAAGTAA

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FIG. 78B

Met Tyr Ser Asn Val Ile Gly Thr Val Thr Ser Gly Lys Arg Lys Val Tyr Leu Leu
Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys His Gly Ser Pro Val Asp
Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn Pro Met Cys Ile Tyr Arg Ser
Pro Glu Lys Lys Ala Thr Glu Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr
Asn Arg Arg Val Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr
Gln His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr Leu Gln Gln
Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys Thr Ser Asp Gln Ile His
Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser
Lys Leu Val Ser Ala Asn Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu
Thr Tyr Gln Asp Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe
Lys Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu Thr Val Leu
Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys Ser Lys Phe Ser Pro Glu
Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser
Met Met Tyr Gln Glu Gly Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln
Val Leu Glu Leu Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys
Pro Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg Phe Arg
Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met Gly Leu Val Asp
Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile Val Ala Glu Gly Arg Asp Asp
Leu Tyr Val Ser Asp Ala Phe His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser
Glu Ala Ala Ala Ser Thr Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg
Val Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys

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FIG. 79A

ATGGATTACTACAGAAAAATATGCAGCTATCTTTCTGGTCACATTGTCTG
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCCCAG
AATGCACGCTACAGGAAAAACCCATTCTTCTCCCAGCCGGGTGCCCA
ATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCA
CTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTCACCTCAGA
GTCCACTTGGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATGGG
GGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTGTT
ATTATCACAAATCTTAA

FIG. 79B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His
Lys Ser

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FIG. 79C

ATGGAGATGTTCCAGGGGCTGCTGCTGTTGCTGCTGAGCATGGGG
GGGACATGGGCATCCAAGGAGCCGCTTCGGCCACGGTGCCGCCCCAT
CAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCGTGTGCATCA
CCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGACCCGCG
TGCTGCAGGGGGTCTTGCCGGCCCTGCCTCAGGTGGTGTGCAACTACC
GCGATGTGCGCTTCGAGTCCATCCGGCTCCCTGGCTGCCGCGCGGGCG
TGAACCCCGTGGTCTCCTACGCCGTGGCTCTCAGCTGTCAATGTGCAC
TCTGCCGCGCGAGCACCCTGACTGCGGGGGTCCAAGGACCACCCC
TTGACCTGTGATGACCCCCGCTTCCAGGACTCCTCTTCTCAAAGGCC
CCTCCCCCAGCCTTCCAAGCCCATCCGACTCCCGGGGCCCTCGGAC
ACCCCGATCCTCC CACAATAA

FIG. 79D

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Ser Met Gly Gly Thr
Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala
Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala Gly
Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val
Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg
Gly Val Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu Cys
Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp
Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser
Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln

FIG. 80A

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ATGCGTCCCCTGCGCCCCCGCGCGCTGCTGGCGCTCCTGGCCTCG
CTCCTGGCCGCGCCCCCGGTGGCCCCGGCCGAGGCCCGCACCTGGT
GCAGGTGGACGCGGCCCGCGCGCTGTGGCCCCCTGCGCGCTTCTGGA
GGAGCACAGGCTTCTGCCCCCGCTGCCACACAGCCAGGCTGACCAG
TACGTCTCTAGCTGGGACCAGCAGCTCAACCTCGCCTATGTGGGCGCC
GTCCCTCACCGCGGCATCAAGCAGGTCCGGACCCACTGGCTGCTGGA
GCTTGTCACCAACCAGGGGGTCCACTGGACGGGGCCTGAGCTACAAC
TCACCCACCTGGACGGGTACTTGGACCTTCTCAGGGAGAACCAGCTCC
TCCCAGGGTTTGAGCTGATGGGCAGCGCCTCGGGCCACTTCACTGACT
TTGAGGACAAGCAGCAGGTGTTTGAGTGGAAGGACTTGGTCTCCAGC
CTGGCCAGGAGATACATCGGTAGGTACGGACTGGCGCATGTTTCCAA
GTGGAACCTTCGAGACGTGGAATGAGCCAGACACACGACTTTGACA
AGCTTCCATGGACATGCAAGGCTTCTGAACTACTACGATCGTGGCTGCT
CGGAGGGTCTGCGCGCCGCCAGCCCCGCCCTGCGGCTGGGAGGCCCC
GGCGACTCCTTCCACACCCACCGCGATCCCCGCTGAGCTGGGGCCTC
CTGCGCCACTGCCACGACGGTACCAACTTCTCACTGGGGAGCGGG
CGTGCGGTGGCTGACATCTCCCTCCACAGGAAGGGTGCAGCGAGCT
CCATCTCCATCTGGAGCAGGAGAAGGTGCTCGCGCAGCAGATCCGG
CAGCTCTTCCCAAGTTCGCGGACACCCCCATTTACAACGACGAGGGC
GACCCGCTGGTGGGCTGGTCCCTGCCACAGCCGTGGAGGGCGGACGT
GACCTACGCGGCCATGGTGGTGAAGGTTCATCGCGCAGCATCAGAACC
TGCTACTGGCCAACACCACCTCCGCCTTCCCCTACGCGCTCCTGAGCA
ACGACAATGCCTTCTGAGCTACCACCCGCACCCCTTCGCGCAGCGCA
CGCTCACCGCGCGCTTCCAGGTCAACAACACCCGCCCGCGCACGTG
CAGCTGTTGCGCAAGCCGGTGCTACGGCCATGGGGCTGCTGGCGCT
GCTGGATGAGGAGCAGCTCTGGGCCGAAGTGTCGCAGGCCGGGACCG
TCCTGGACAGCAACCACACGGTGGGCGTCTGGCCAGCGCCACCGC
CCCCAGGGCCCGGCCGACGCTGGCGCGCCGCGGTGCTGATCTACGC
GAGCGAGCAGACCCGCGCCACCCCAACCGCAGCGTGCAGGTGACCC
TGCGGCTGCGCGGGGTGCCCCCGGCCCGGGCCTGGTCTACGTACG
CGCTACCTGGACAACGGGCTCTGCAGCCCCGACGGCGAGTGGCGGGC
CCTGGGCGCGCCGCTTCCCCACGGCAGAGCAGTTCGGCGCATCG
GCGCGGTGAGGACCGCGGTGGCGCGCGCGCCCGCCCTTACCCGCC
GGCGCGCGCCTGACCTGCGCCCCGCGCTGCGGCTGCCGTGCTTTG
CTGGTGACAGTGTGTGCGCGCCCCGAGAAGCCGCCCGGGCAGGTAC
GCGGCTCCGCGCCCTGCCCTGACCCAAGGGCAGCTGGTTCTGGTCTG
GTCGGATGAACACGTGGGCTCCAAGTGCTGTGGACATACGAGATCC
AGTTCTCTCAGGACGGTAAGGCGTACACCCCGGTACGAGGAAGCCA
TCGACCTTCAACCTCTTTGTGTTACGCCAGACACAGGTGCTGTCTCT
GGCTCCTACCGAGTTCGAGCCCTGGACTACTGGGCCCCGACCAGGCC
CTTCTCGGACCCTGTGCCGTACCTGGAGGTCCCTGTGCCAAGAGGGCC
CCCATCCCCGGGCAATCCATGA

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FIG. 80B

Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Ser Leu Leu
 Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val Gln Val Asp Ala Ala
 Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe Cys Pro Pro Leu
 Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala
 Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu
 Glu Leu Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr His
 Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro Gly Phe Glu
 Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp Lys Gln Gln Val
 Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg Arg Tyr Ile Gly Arg Tyr Gly
 Leu Ala His Val Ser Lys Trp Asn Phe Glu Thr Trp Asn Glu Pro Asp His His Asp
 Phe Asp Asn Val Ser Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys
 Ser Glu Gly Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
 Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys His Asp
 Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp Tyr Ile Ser Leu His
 Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu Gln Glu Lys Val Val Ala Gln
 Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala
 Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala
 Ala Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr Thr
 Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His Pro
 His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg
 Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu Ala
 Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu
 Asp Ser Asn His Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala
 Asp Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro
 Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu
 Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp
 Arg Arg Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln Phe Arg Arg Met Arg
 Ala Ala Glu Asp Pro Val Ala Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu
 Thr Leu Arg Pro Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala
 Arg Pro Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln
 Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp Thr
 Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val Ser Arg Lys Pro
 Ser Thr Phe Asn Leu Phe Val Phe Ser Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr
 Arg Val Arg Ala Leu Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro
 Tyr Leu Glu Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro

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FIG. 81A

ATGCAGCTGAGGAACCCAGAACTACATCTGGGCTGCGCGCTTGCGCT
TCGCTTCCTGGCCCTCGTTTCCTGGGACATCCCTGGGCTAGAGCACT
GGACAATGGATTGGCAAGGACGCCTACCATGGGCTGGCTGCACTGGG
AGCGCTTCATGTGCAACCTTGACTGCCAGGAAGAGCCAGATTCTTGC
ATCAGTGAGAAGCTCTTCATGGAGATGGCAGAGCTCATGGTCTCAGA
AGGCTGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGACTGTTG
GATGGCTCCCCAAAGAGATTGAGAAAGCAGACTTCAGGCAGACCCTC
AGCGCTTTCCTCATGGGATTGCGCAGCTAGCTAATTATGTTACAGCA
AAGGACTGAAGCTAGGGATTTATGCAGATGTTGGAAATAAAACCTGC
GCAGGCTTCCCTGGGAGTTTTGGATACTACGACATTGATGCCAGACC
TTTGCTGACTGGGGAGTAGATCTGCTAAAATTGATGGTTGTTACTGT
GACAGTTTGGAATAATTGGCAGATGGTTATAAGCACATGTCCTTGGCC
CTGAATAGGACTGGCAGAAGCATTGTGTACTCCTGTGAGTGGCCCTCTT
TATATGTGGCCCTTTCAAAGCCCAATTATACAGAAATCCGACAGTAC
TGCAATCACTGGCGAAATTTTGCTGACATTGATGATTCCCTGGAAAAGT
ATAAAGAGTATCTTGGACTGGACATCTTTTAACCAGGAGAGAATTGTT
GATGTTGCTGGACCAAGGGGTTGGAATGACCCAGATATGTTAGTGAT
TGGCAACTTTGGCCTCAGCTGGAATCAGCAAGTAACTCAGATGGCCCT
CTGGGCTATCATGGCTGCTCCTTTATTCATGTCTAATGACCTCCGACA
CATCAGCCCTCAAGCCAAAGCTCTCCTTCAGGATAAGGACGTAATTGC
CATCAATCAGGACCCCTTGGGCAAGCAAGGGTACCAGCTTAGACAGG
GAGACAAGTTTGAAGTGTGGGAACGACCTCTCTCAGGCTTAGCCTGG
GCTGTAGCTATGATAAACCGGCAGGAGATTGGTGGACCTCGCTCTTAT
ACCATCGCAGTTGCTTCCCTGGGTAAAGGAGTGGCCTGTAATCCTGCC
TGCTTCATCACACAGCTCCTCCTGTGAAAAGGAAGCTAGGGTTCTAT
GAATGGACTTCAAGGTTAAGAAGTCACATAAATCCACAGGCACTGT
TTTGCTTCAGCTAGAAAATACAATGCAGATGTCAATAAAGACTTACT
TTAA

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FIG. 81B

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg Phe
Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp Asn Gly Leu Ala
Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg Phe Met Cys Asn Leu Asp
Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser Glu Lys Leu Phe Met Glu Met Ala Glu
Leu Met Val Ser Glu Gly Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp
Cys Trp Met Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln
Arg Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu Lys
Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe Pro Gly Ser Phe
Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp Trp Gly Val Asp Leu Leu Lys
Phe Asp Gly Cys Tyr Cys Asp Ser Leu Glu Asn Leu Ala Asp Gly Tyr Lys His
Met Ser Leu Ala Leu Asn Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro
Leu Tyr Met Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser Ile Leu
Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala Gly Pro Gly Gly Trp
Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe Gly Leu Ser Trp Asn Gln Gln
Val Thr Gln Met Ala Leu Trp Ala Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp
Leu Arg His Ile Ser Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala
Ile Asn Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met Ile Asn
Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val Ala Ser Leu Gly Lys
Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr Gln Leu Leu Pro Val Lys Arg Lys
Leu Gly Phe Tyr Glu Trp Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr
Val Leu Leu Gln Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu

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FIG. 82A

ATGGCGCCCGTCGCCGCTCTGGGCCGCGCTGGCCGTCGGACTGGAGCT
CTGGGGTGGCGGCGACGCCCTTGCCCCGCCAGGTGGCATTACACCCTA
CGCCCCGAGCCCGGGAGCACATGCCGGCTCAGAGAATACTATGACC
AGACAGCTCAGATGTGCTGCAGCAAATGCTCGCCGGGCCAACATGCA
AAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAG
GACAGCACATACACCCAGCTCTGGAAGTGGGTTCGGAGTGCTTGAG
CTGTGGCTCCCGCTGTAGCTCTGACCAGGTGGAACTCAAGCCTGCAC
TCGGGAACAGAACCGCATCTGCACCTGCAGGCCCGGCTGGTACTGCG
CGCTGAGCAAGCAGGAGGGGTGCCGCTGTGCGCGCCGCTGCGCAAG
TGCCGCCCCGGGCTTCGGCGTGCCAGACCAGGAACTGAAACATCAGA
CGTGGTGTGCAAGCCCTGTGCCCCGGGGACGTCTCCAACACGACTTC
ATCCACGGATATTTGCAGGCCCCACCAGATCTGTAACGTGGTGCCAT
CCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCA
CCCGGAGTATGGCCCEAGGGGCAGTACACTTACCCAGCCAGTGTCC
ACACGATCCCAACACACGCAGCCAACTCCAGAACCAGCACTGTCTC
AAGCACCTCCTTCTGTCTCCAATGGGCCCCAGCCCCCAGCTGAAGG
GAGCATCTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGTGAC
AGCCTTGGGTCTACTAATAATAGGAGTGGTGAAGTGTGTCATCATGAC
CCAGGTGAAAAAGAAGCCCTTGTGCCTGCAGAGAGAAGCCAAGGTGC
CTCACTTGCTGCCGATAAAGGCCCGGGGTACACAGGGCCCCGAGCAG
CAGCACCTGTGATCACAGCGCGAGCTCCAGCAGCAGCTCCCTGGA
GAGCTCGGCCAGTGCGTTGGACAGAAGGGCGCCCACTCGGAACCAGC
CACAGGCACACAGGCGTGGAGGCCAGTGGGGCCGGGGAGGCCCGGGC
CAGCACCGGGAGCTCAGATTCTTCCCCTGGTGGCCATGGGACCAAGG
TCAATGTCACTGCATCGTGAACGTCTGTAGCAGCTCTGACCACAGCT
CACAGTGCTCCTCCCAAGCCAGCTCCACAATGGGAGACACAGATTCC
AGCCCCTCGGAGTCCCCGAAGGACGAGCAGGTCCCCCTTCTCCAAGGA
GGAATGTGCCTTTCGGTCCAGCTGGAGACGCCAGAGACCCCTGTGG
GGAGACCCGAAGAGAAGCCCTGCCCTTGGAGTGGCTGATGCTGGG
ATGAAGCCCAGTTAACCAAGGCCGGTGTGGGCTGTGTCTGAGCCAAGG
TGGGCTGAGCCCTGGCAGGATGACCCTGCGAAGGGGCCCTGGTCCTT
CCAGGC

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FIG. 82B

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala
Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys
Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln
Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val
Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr
Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val
Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr
Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln
His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro
Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly
Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val
Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro
His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg
Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly
Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln
Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys
Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu
Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro
Asp Ala Gly Met Lys Pro Ser

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FIG. 83A

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

FIG. 83B

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr
Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys
Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
Gly Thr Leu Val Thr Val Ser Ser

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FIG. 84A

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr
Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Ser Val Gly Trp
Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp
Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr
Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly
Thr Thr Val Thr Val Ser Ser

FIG. 84B

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met His Trp Tyr Gln Gln Lys
Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser
Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 85A

GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGA
 GAAAGAGTCAGTTTCTCCTGCAGGGCCAGTCAGTTCGTGGCTCAAGC
 ATCCACTGGTATCAGCAAAGAACAATGGTTCTCCAAGGCTTCTCATA
 AAGTATGCTTCTGAGTCTATGTCTGGGATCCCTTCCAGGTTTAGTGCC
 AGTGGATCAGGGACAGATTTTACTCTTAGCATCAACACTGTGGAGTCT
 GAAGATATTGCAGATTATTACTGTCAACAAAGTCATAGCTGGCCATTC
 ACGTTCGGCTCGGGGACAAATTTGGAAGTAAAAGAAGTGAAGCTTGA
 GGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCT
 CCTGTGTTGCCTCTGGATTCAATTTTCAGTAACCACTGGATGAAGCTGGG
 TCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTGCTGAAATTAGA
 TCAAAATCTATTAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGG
 AGGTTCAACATCTCAAGAGATGATTCCAAAAGTGCTGTCTACCTGCAA
 ATGACCGACTTAAGAACTGAAGACACTGGCGTTTATTACTGTTCCAGG
 AATTACTACGGTAGTACCTACGACTACTGGGGCCAAGGCACCACTCTC
 ACAGTCTCC

FIG. 85B

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly Glu Arg Val
 Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser Ile His Trp Tyr Gln Gln
 Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Met Ser Gly
 Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
 Thr Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro
 Phe Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu Glu Ser
 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser Cys Val Ala Ser Gly
 Phe Ile Phe Ser Asn His Trp Met Asn Trp Val Arg Gln Ser Pro Gly Lys Gly Leu
 Glu Trp Val Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr
 Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg
 Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser

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FIG. 86A

ATGGAGACAGACACACTCCTGTTATGGGTGCTGCTGCTCTGGGTTC
CAAGTTCCACTGGTGACGTCAGGCGAGGGCCCCGGAGCCTGCGGGGCAG
GGACGCGCCAGCCCCACGCCCTGCGTCCCGGCCGAGTGCTTCGACC
TGCTGGTCCGCCACTGCGTGGCCTGCGGGCTCCTGCGCACGCCGCGGC
CGAAACCGGCCGGGGCCAGCAGCCCTGCGCCAGGACGGCGCTGCAG
CCGCAGGAGTCGGTGGGCGCGGGGGCCGGCGAGGCGGCGGTCGACA
AAACTCACACATGCCCCACGTGCCAGCACCTGAACTCCTGGGGGA
CCGTAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATC
TCCCGGACCCCTGAGGTACATGCGTGGTGGTGACGTGAGCCACGA
AGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGAGGTGC
ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA
CCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAAGGACTGGCTGAATGG
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA
TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG
GTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGT
CAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGT
GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAATAAGACCACG
CCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTC
ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTC
CGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT
CCCTGTCTCCCGGAAATGA

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FIG. 86B

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser
Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg Asp Ala Pro Ala
Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu Leu Val Arg His Cys Val Ala
Cys Gly Leu Leu Arg Thr Pro Arg Pro Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro
Arg Thr Ala Leu Gln Pro Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

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FIG. 87

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val
 Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
 Lys Pro Asp Gly Ile Val Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser
 Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
 Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

FIG. 88

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr Ser Val Arg
 Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Lys
 Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
 Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
 Thr Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe
 Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly Thr
 Leu Val Thr Val Ser Ala

FIG. 89

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
 Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
 Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
 Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu
 Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys

FIG. 90

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
 Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg
 Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
 Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser
 Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
 Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 Thr Leu Val Thr Val Ser Ser

FIG. 91

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Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
 Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
 Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
 Ser Leu Gln Pro Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu
 Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala Pro
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
 Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
 Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 Ser Phe Asn Arg Gly Glu Cys

FIG. 92

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
 Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg
 Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
 Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser
 Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
 Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

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FIG. 93A

ATGGATTTTCAGGTGCAGATTATCAGCTTCCTGCTAATCAGTGCTTCA
GTCATAATGTCCAGAGGGCAAATTGTTCTCTCCAGTCTCCAGCAATC
CTGTCTGCATCTCCAGGGGAGAAGGTCACAATGACTTGCAGGGCCAG
CTCAAGTGTAAGTTACATCCACTGGTTCAGCAGAAGCCAGGATCCTC
CCCCAAACCCTGGATTATGCCACATCCAACCTGGCTTCTGGAGTCCC
TGTTGCTTCAGTGGCAGTGGGTCTGGGACTTCTTACTCTCTCACAAT
CAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGT
GGACTAGTAACCCACCCACGTTCCGGAGGGGGACCAAGCTGGAAATC
AAA

FIG. 93B

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser Val Ile Met Ser
Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly Glu
Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile His Trp Phe Gln
Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser
Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn
Pro Pro Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 94A

ATGGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTG
TCCTGTCCCAGGTACAACCTGCAGCAGCCTGGGGCTGAGCTGGTGAAG
CCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACATT
ACCAGTTACAATATGCACTGGGTAAAACAGACACCTGGTCGGGGCCT
GGAATGGATTGGAGCTATTTATCCCGAAATGGTGATACTTCCTACAA
TCAGAAGTTCAAAGGCCAAGGCCACATTGACTGCAGACAAATCCTCCA
GCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCG
GTCTATTACTGTGCAAGATCGACTTACTACGGCGGTGACTGGTACTTC
AATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCTGCA

FIG. 94B

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg Val Leu Ser
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys
Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp
Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly
Thr Thr Val Thr Val Ser Ala

FIG. 95A

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GACGTCGCGGCCGCTCTAGGCCTCCAAAAAGCCTCCTCACTACTTCT
GGAATAGCTCAGAGGCCGAGGCGCCTCGGCCCTGTCATAAAATAAAA
AAAATTAGTCAGCCATGCATGGGGCGGAGAATGGGCGAACTGGGCG
GAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCT
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCT
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGC
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGA
CACACATTCCACAGAATTAATTCCTAGTTATTAATAGTAATCAATT
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAA
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCGCCC
ATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA
CTTTCCATTGACGTCAATGGGTGGACTATTACGGTAAACTGCCCACT
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG
TGAACGCGGTAAATGGCCCGCCTGGCATTATGCCAAGTACGCGGCTG
TATGGGACTTTCTACTTTGGCAGTACATCTACGTATTAGTCATCGCTA
TTACCATGGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATAGC
GGTTTGACTCACGGGGATTTCGAAGTCTCCACCCCAATTGACGTCAATG
GGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGCTGTA
ACAACTCCGCCCCATTGACGCAAAATGGGCGGTAGGCGTGTACGGTGG
GAGGTCTATATAAGCAGAGCTGGGTACGTGAACCGTCAGATCGCCTG
GAGACGCCATCACAGATCTCTACCATGAGGGTCCCCGCTCAGCTCCT
GGGGCTCCTGTGCTCTGGCTCCAGGTGCACGATGTAGTGGTACCAA
GGTGGAATCAAACTGACGGTGGCTGCACCATCTGTCTTCATCTTCCC
GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCT
GCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGG
ATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAG
GACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAG
CAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAAGTCAACC
ATCAGGGCCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAG
TGTGAATTCAGATCCGTTAACGGTTACCAACTACCTAGACTGTGATT
GTGACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTG
CCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCTTCTCT
TGACCCCTGGAAGGTGCCACTCCCACTGTCTTTTCTTAATAAAATGAGG
AAATTGTCATCGAATTGTCTGAGTAGGTGTCATTTCTATTCTGGGGGTG
GGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAG
GCATGCTGGGGATGCGGTGGGCTCTATGGAACCAAGCTGGGGCTCGAC
ACGTATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGC
CCGCTGGCATTTATGCCAGTACATGACCTTATGGGACTTTGGCTACTT
GGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGT
TTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGA
TTTCCAAGTCTCCACCCCAATTGACGTCAATGGGAGTTTGTGTTGGCAC

FIG. 95B

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CAAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCATTG
ACGCAAAATGGGCGGTAGGCGGTGTACGGTGGGAGGTCTATATAAGCAG
AGCTGGGTACGTCTTCACATTCAAGTATCAGCACTGAACACAGACCC
GTGACATGGGTGGGAGCCTCATCTTGCTCTTCTTGTGCGTGTGCTA
CGCGTGTCCGTAAGCACCAAGGGCCATCGGTCTTCCCCCTGGCACCCCT
CCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCGAACC GGGTGACGGTGTCTGTGGAACCTCAGGCGC
CCTGACCAGCGCGGTGCACACCTTCCCGGCTGTCTACAGTCTCAGG
ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGGTTGGG
CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCA
AGGTGGACAAGAAAGCAGAGGCCAAAATCTTGTGACAAAACCTACACA
TGCCCCACCGTGCCACGACCTGAACTCCTGGGGGGACCGTCACTCTTC
CTCTCCCGCTCAGCACGACCCCTCATGATCTCTCCGTCAGGCTGGG
GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA
CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTTCAGG
GTCTCACCCTCCTGACACGAGGACTGGCTGAATGGCAAGGATACAA
GTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCA
TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCCACAGGTGTACACCCTG
CCCCATCCCGGGATGAGCTGACCAGGAACAGGTGACCGCTGACCTG
CGCTCTGCACAAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
GCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCCTGGACAAG
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGA
GGCTCTGCACAAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
TAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTCTGT
ACAATATGCGGCCCGTGATATCTACGTATGATCAGCCTCGACTGTGCCT
TCTAGTTGCCAGCCATCTGTTGTTGGCCCTCCCCCGTGCCCTCCTTGA
CCTTGAAGGTGCCACTCCCACTGTCTTCTTCTAATAAAATGAGGAAA
TTGCATCGCATTGTCTGAGTAGGTGTCTATTCTATTCTGGGGGTGGGG
TGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCA
TGCTGGGGATGCGGTGGGCTCTATGGAAACAGCTGGGGCTCGACAGC
GCTGGATCTCCCGATCCCCAGCTTGTCTCTCAATTTCTTAATTGCTA
ATGAGAAAAAAAGGAAAAATTAATTTTAACACCAATTCACTAGTTGAT
TGAGCAAAATGCGTTGCCAAAAAGGATGCTTAGAGACAGTGTCTCT
GCACAGATAAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG
ACTCCTAAGCCAGTGAAGTGGCACAGCATTCTAGGGAGAAAATATGCTT
GTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCC
AATCTGCTCACACAGGATAGAGAGGGGCAGGAGCCAGGGCAGAGCAT
ATAAGGTGAGGTAGGATCAGTTGCTCTCACATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGG

FIG. 95C

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GCTGCGATTTCGCGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTG
GTAGGATTTTATCCCCGCTGCCATCATGGTTCGACCATTGAACTGCAT
CGTCGCCGTGTCCCAAAATATGGGGATTGGCAAGAACGGAGACCTAC
CCTGGCCTCCGCTCAGGAACGAGTTCAAGTACTTCCAAAGAATGACC
ACAACCTCTTCAGTGGGAAGGTAAACAGAAATCTGGTGATTATGGGTAG
GAAAACCTGGTTCTCCATTCTGAGAACAAATCGACCTTTAAAGGACA
GAATTAATATAGTTCTCAGTAGAGAACTCAAAGAACCACCACGAGGA
GCTCATTTTCTTGCCAAAAGTTTGGATGATGCCTTAAGACTTATTGAA
CAACCGGAATTGGCAAGTAAAGTAGACATGGTTTGGATAGTCGGAGG
CAGTTCTGTTTACCAGGAAGCCATGAATCAACCAGGCCACCTTAGACT
CTTTGTGACAAGGATCATGCAGGAATTTGAAAGTGACACGTTTTTCCC
AGAAATTGATTGGGGAAATATAAACTTCTCCAGAATACCCAGGCG
TCTCTCTGAGTCCAGGAGGAAAAAGGCATCAAGGTAGTCCACTCCCAG
GTCTACGAGAAGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCTGC
TCCCTCCTAAAGTCATGCATTTTTATAAGACCATGGGACTTTTGCTG
GCTTTAGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTGTG
TGCCCTCCCCGCTGCCTTCTTGACCTGGAAGGTGCCACTCCCAC
TGTCCTTTCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAG
GTGTCAATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGG
AGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCT
ATGGAACCAAGCTGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTT
ATTTGCATAATGAGAAAAAAAGGAAAATTAATTTTAAACCAATTCA
GTAGTTGATTGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACA
GTGTTCTCTGCACAGATAAGGACAAACATTATTCAGAGGGAGTACCC
AGAGCTGAGACTCCTAAGCCAGTGAGTGGCACAGCAATTCTAGGGAGA
AATATGCTTGTCTATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGG
TAAGGGCCAATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGG
CAGAGCATATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTC
TGACATAGTTGTGTTGGGAGCTTGATCGATCCTCTGATGGTTGAACAA
GATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCT
GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGT
GTCCGGCTCTCAGCGCAGGGGCGCCCGTTCTTTTGTCAAGACCGA
CCTGTCCGGTCCAGCTGAATGAACTGCAGGACGAGGACGCGCGCTAT
CGTGGCTGGCCACGACGGGCGTTTCTTGCGCAGCTGTGCTCGACGTTG
TCACTGAAGCGGGAAAGGACTGGCTGCTATTGGGCGAAGTGCCCGGG
CAGGATCTCTGTCTATCTACCTTGCTCTGCGGAGAAAGTATCCATC
ATGGCTGATGCAATGCGGGCGGTGCATACGCTTGATCCGGTACCTGCG
CCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTAATCG
GATGGAAGCCGGTCTTGTCGATCAGGATGATCTGAGCAAGAGCATC
AGGGGCTCGCGCAGCGCAAGCTTGCCAGGCTCAAGCGCGCATG
CCCGACGGCGAGGATCTCGTCTGTGACCCATGGCGATGCTGCTTGGCG

FIG. 95D

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AATATCATGGTGGAAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGC
CGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCG
TGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCTCGT
GCTTTACGGTATCGCCGCTTCCCGATTTCGCAGCGCATCGCCTTCTATC
GCCTTCTTGACGAGTTCCTCTGAGCGGGAAGCTGCGGTTTCGAAATGAC
CGACCAAGCGACGCCCAACCTGCCATCAGGAGATTTTCGATTCCACCG
CCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTCCGGGACGCGG
GCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCC
ACCCCAACTTGTATTGTCAGCTTATAATGGTTACAAATACAAAGCAATA
GCATCAGAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTT
GTGGTTTGTCCAAACTCATCAATCTATCTATCATGTCTGGATCGCGG
CCGCGATCCCGTCGAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCC
TGTGTGAAATTGTTATTCGCTCACAAATCCACAGGATACAAAGCCGG
AGCATAAAGTGTAAGGCTGGGGTGCCTAATGAGTGAGCTAACTCAC
ATTAATTGCGTTGCGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTC
GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT
TGCGTATTGGCGCTCTTCCGCTTCTCGCTCACTGATCGTCTGCGCTC
GGTCGTTCCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAA
TACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA
GCAAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGC
TGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAATC
GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAC
CAGGCGTTTTCCCGCTGGAAGCTCCCTCGTGCCTCTCTCTGTTCCGACC
CTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTG
GCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCCGTGTAGGTC
GTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGCTTCAGCCCGAC
CGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGA
CAOGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG
AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA
ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGA
AGCCAGTTACCTTCGGAAGAAAGAGTTGGTAGCTCTTGATCCGGCAAA
CAAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATT
ACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC
GGGGTCTGACGCTCAGTGGAACGAAACTCACGTAAAGGGATTTTGG
TCATGAGATTATCAAAAAGGATCTTCACTAGATCCTTTTAAATTAATA
AATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTG
ACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTC
TATTTCTGTTTCATCCATAGTTGCCCTGACTCCCCGTCGTGTAGATAACTAC
GATACGGGAGGGCTTACCATCTGCCCCAGTGCTGCAATGATACCGC
GAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACACGCCA
GCCGGAAGGGCCGAGCGCAGAAAGTGGTCCTGCAACTTTATCCGCCTC
CATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGC

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FIG. 95E

CAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGG
TGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAAC
GATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTT
AGCTCCTTCGGTCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTG
TTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGC
CATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCAT
TCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAA
TACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAAGTGCTCATC
ATTGGAACCGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTG
TTGAGATCCAGTTCGATGTAAACCACTCGTGACCCAACTGATCTTCA
GCATCTTTTACTTTCACCAAGCGTTTCTGGGTGAGCAAAAAACAGGAAGG
CAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAA
TACTCATACTCTTCTTTTCAATATTATTGAAGCATTTATCAGGGTTA
TTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACA
AATAGGGGTTCCGCGCACATTCCCCGAAAAGTGCCACCT

FIG. 96A

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GACGTCGCGGCCGCTCTAGGCCTCCAAAAAGCCTCCTCACTACTTCT
GGAATAGCTCAGAGGCCGAGGCGGCCTCGCCTCTGCATAAATAAAA
AAAATTAGTCAGCCATGCATGGGGCGGAGAATGGGCGGAACTGGGCG
GAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCT
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCT
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGC
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACCTGA
CACACATTCCACAGAATTAATTCCCCTAGTTATTAATAGTAATCAATT
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGGTACATAA
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGCCCGCCCC
ATTGACGTCATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA
CTTTCCATTGACGTCATAGGGTGGACTATTTACGGTAACTGCCCACT
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG
TGCAATGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATGACCT
TATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTA
TTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATACC
GGTTTGACTCAGCGGATTTCGAAGTCTCCACCCCAATTGACGTCATG
GGAGTTGTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAAATGTCGTA
ACAACTCCGCCCCATTGACGCAAAATGGGCGGTAGGCGTGTACGGTGG
GAGGTCTATATAAGCAGAGCTGGGTACGTGAACCGTCAGATCGCCTG
GAGACGCCATCAGATCTCTCACTATGGATTTTCAGGTGCAGATTAT
CAGCTTCCTGCTAATCAGTGCTTCAGTCATAATGTCCAGAGGACAAAAT
TGTTCTCTCCCACTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAA
GGTCACAAATGACTTGACAGGGCCAGCTCAAGTGTAAGTTACATCCACT
GGTTCCAGCAGAAGCCAGGATCCTCCCCCAAAACCTGGATTATGCCA
CATCCAACCTGGCTTCTGGAGTCCCTGTTTCGCTTCAGTGGCAGTGGGT
CTGGGACTTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATG
CTGCCACTTATTACTGCCAGCAGTGGACTAGTAACCCACCCACGTTTCG
GAGGGGGGACCAAGCTGGAATCAAACGTACGGTGGCTGCACCATCT
GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATGCTG
TCTGTTGTGTGCTGCTGAATAACTTCTATCCCAGAGAGGGCCAAAGTA
CAGTGGAAAGGTGGATAACGCCTCCAATCGGGTAACTCCAGGAGAG
TGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCA
CCCTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTACGCC
TGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTT
CAACAGGGGAGAGTGTGTAATTCAGATCCGTTAACGGTTACCAACTA
CCTAGACTGGATTCTGTGACAACATGCGGCCGTGATATCTACGTATGAT
CAGCCTCGACTGCGCCTTCTAGTTGCCAGCCATCTGTGTTTGGCCCTC
CCCCGTGCCTTCCTTGACCTGGAAAGGTGCCACTCCCACTGTCTTTCC

FIG. 96B

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TAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCT
ATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGG
AAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCA
GCTGGGGCTCGACAGCTATGCCAAGTACGCCCCCTATTGACGTCAATG
ACGGTAAATGGCCGCTGGCATTATGCCAGTACATGACCTTATGGG
ACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCAT
GGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTTG
ACTCACGGGGATTTCGAAGTCTCCACCCCATTTGACGTCAATGGGAGTT
TGTTTTGGCACCAAAATCAACGGGACTTTCAAAAATGTCGTAACAACT
CCGCCCCATTGACGCAAAATGGGCGGTAGGCGGTGACGGTGGGAGGTC
TATATAAGCAGAGCTGGGTACGTCTCACATTCACTGATCAGCACTGA
ACACAGACCCGTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGT
CGCTGTGTGCTACCGGTGTCCTGTCCAGGTACAACCTGCAGCAGCCTGG
GGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGCTCGTGAAGG
CTTCTGGCTACACATTTACCAAGTTACAATATGCACTGGGTAACACAGA
CACCTGGTGGGGGCTGGAATGGATTGGAGCTATTATCCCGGAAAT
GGTGATACTTCCATAACAATCAGAAGTTCAAAGGCAAGGCCACATTGAC
TGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGA
CATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACG
GCGGTGACTGGTACTTCAATGTCTGGGGCGCAGGGACCCAGGTCACC
GTCTCTGAGCTAGCACCAAGGGCCCATCGGTCTTCCCTTGGCACCC
TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT
CAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCG
CCCTGACCAGCGCGGTGCACACCTTCCCGGCTGTCTACAGTCTCTAG
GACTCTACTCCTCAGCAGCGTGGTGACCGTGCCCTCAGCAGCTTGG
GCACCCAGACCTACATCTGCAACGTGAATCACAAGCCAGCAACACC
AAGGTGGACAAGAAAGCAGAGCCCCAAATCTTGTGACAAAACCTCACAC
ATGCCCACCGTGCCACGACCTGAACTCCTGGGGGGACCGTCAGTCTT
CTCTTCTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCC
TGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGG
TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAG
ACAAAGCCGGGGAGGAGCAGTACAACAGCAGTACCGTGTGGTTCAG
CGTCTCAGCGTCTGCAACGAGACTGGCTGAATGGCAAGGAGTACA
AGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCAGAAAAACC
ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCT
GCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGACGCTGACCT
GCCTGGTCAAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAG
AGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCT
GGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCCTGGACAA
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCAATG
AGGCTCTGCACAACCACTACACGACAGAAAGAGCTTCCCTGTCTCCGG
GTAATGAGGATCCGTAAACGGTTACCAACTACCTAGACTGGATTCTCGT

FIG. 96C

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GACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGAGTGTGCC
TTCTAGTTGCCAGCCATCTGTTGTTTGCCCTCCCCGTGCCTTCCTTG
ACCCTGGAAGGTGCCACTCCCAGTGTCTTCTCTAATAAAATGAGGAA
ATTGCATCGCATTTGTCTGAGTAGGTGTCTATTCTTGGGGGGTGGG
GTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGC
ATGCTGGGGATGCGGTGGGCTCTATGGAACCAAGCTGGGGCTCGACAG
CGCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTATTGTCAT
AATGAGAAAAAAGGAAAAATTAATTTTAACACCAATTCAGTAGITGA
TTGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTCTCT
GCACAGATAAGGACAAACATTATTACAGAGGGAGTACCCAGAGCTGAG
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAAATATGCTT
GTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCC
AATCTGCTCACACAGGATAGAGGGCAGGAGCCAGGGCAGGACAGCAT
AATAGGTGAGGTAGGATCAGTTGCTCTCTCACATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGGGCTGCGATTTCG
CGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTGGTAGGATTTTATC
CCCGCTGCCATCATGGTTCGACCATTGAACTGCATCTCGCGGTGTCCT
CAAAATATGGGGATTGGCAAGAACGGAGACCTACCCTGGCCTCCGCT
CAGGAACGAGTTCAAGTACTTCCAAAGAATGACCACAACCTCTTCAG
TGGAAGGTAAACAGAACTCTGGTGATTATGGGTAGGAAAACTGGTTC
TCCATTCTTGAGAAGAATCGACCTTTAAAGGACAGAAATTAATATGTT
CTCAGTAGAGAACTCAAAGAACCACCAGGAGCTCATTTTCTTGC
CAAAAGTTTGGATGATGCCTTAAGACTTATTGAACAACCGGAATTGG
CAAGTAAAGTAGACATGGTTTGGATAGTCGGAGGCAGTTCTGTTTACC
AGGAAGCCATGAATCAACCAGGCCACCTTAGACTCTTTGTGACAAGG
ATCATGCAGGAATTTGAAAGTGACACGTTTTTCCCAGAAATTGATTTG
GGGAAATATAAACTTCTCCCAGAATACCCAGGCGTCTCTCTGA
GGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAAGTCTACGAGA
AGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCTGCTCCCCCTCTAA
AGCTATGCATTTTATAAGACCATGGGACTTTTGCTGGCTTTAGATCA
GCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCTCCC
CCGTGCCTTCTTGACCCTGGAAGGTGCCACTCCCAGTGCCTTTCTCTA
ATAAAATGAGGAAATTCATCGCATGTCTGAGTAGGTTGATGTTCTAT
TCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAA
GACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCAGC
TGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTTATTTCGATAATG
AGAAAAAAGGAAAAATTAATTTTAACACCAATTCAGTAGTTGATTGA
GCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTCTCTGCA
CAGATAAGGACAAACATTATTACAGAGGAGTACCCAGAGCTGAGACT
CCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAAATATGCTTGTG
ATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCCAAT
CTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCATATA
AGGTGAGGTAGGATCAGTTGCTCTCACATTTGCTTCTGACATAGTTG

FIG. 96D

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TGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAAGATGGATTGCA
CGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTCGGCTATGACTG
GGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCGGGCTGTC
AGCGCAGGGGCGCCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGC
CCTGAATGAACTGCAGGACGAGGCAGCGCGGTATCGTGGCTGGCCA
CGACGGGCGTTTCCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCCGG
GAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTG
TCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCA
ATCGCGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCAC
CAAGCGAAACATCGCATCGAGCGAGCAGTACTCGCATGGAAAGCCGG
TCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGC
CAGCCGAACCTGTTCCGCCAGGCTCAAGCGCGCATGCCCGACGGCGAG
GATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTG
GAAAAATGGCCGCTTTTCTGGATTCACTGTGGCCGGCTGGGTGTG
GCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGA
AGAGCTTGGCGGCAATGGGCTGACCGCTTCTCGTGCTTTACGGTAT
CGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCTTCTTGACGA
GTTCTTCTGACGCGGAATCTGGGGTTCGAAATGACCGCAACGCGAC
GCCCAACCTGCCATCAGGATTTTCGATTCCACCGCCGCTTCTATGA
AAGTTGGGCTTCGGAATCGTTTTCGGGACGCCGGCTGGATGATCCT
CCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCCAACTTGTT
TATTCGAGCTTATAATGGTTACAAATAAAGCAATAGCATCAGAAATTT
CACAAATAAAGCATTTTTTCACTGCATTCTAGTTGTGGTTGTCCAA
ACTCATCAATCTATCTTATCATGTCTGGATCGCGGCCGCGATCCCGTC
GAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTGT
TATCCGCTCACAAATTCACACAACATACGAGCCGGAAGCATAAAGTG
TAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTT
GCGCTCACTGCCGCTTTCAGTCGGGAAACCTGTCGTGCCAGCTGCA
TTAATGAATCGGCCAACGCGCGGGGAGAGCGGTTTGCGTATTGGGC
GCTCTTCGCTTCTCGCTCACTGACTCGCTGCGCTCGCTGTTTCGGCT
GCGGCGAGCGGTATCAGCTCACTCAAAGCGGTAATACGGTTATCCA
CAGAAATCAGGGGATAACGCAAGGAAAGAACATGTGAGCAAAAGGCCA
GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGTGGCGTTTTTCC
ATAGGCTCCGCCCCCTGACGAGCATCAGAAATCGACGCTCAAGT
CAGAGGTGGCGAAACCGACAGGACTATAAAGATACCAGGCGTTTCC
CCTGGAAGTCTCCCTCGTGCCTCTCCTGTTCCGACCTGCGCGTTAC
CGGATACCTGTCCGCCCTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA
ATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAA
GCTGGGCTGTGTGACGAACCCCGGTTACGCCGACCGCTGCGCCTT
ATCCGGTAACATATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC

FIG. 96E

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GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATG
TAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC
ACTAGAAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC
TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGC
TGGTAGCGGTGGTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAA
AAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGC
TCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGAGATTATC
AAAAAGGATCTTCACCTAGATCCTTTTAAATTAATAAATGAAGTTTAA
ATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATG
CTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCC
ATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGG
CTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTC
ACCGGCTCCAGATTTATCAGCAATAAACCCAGCCAGCCGAAGGGCCG
AGCGCAGAAAGTGGTCTGCAACTTTATCCGCCTCCATCCAGTCTATTA
ATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGC
GCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCTGT
TTGGTATGGCTTCATTAGCTCCGGTTCCCAACGATCAAGGCGAGTTA
CATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTC
CGATCGTTGTGTCAGAAAGTAAGTTGGCCGCGAGTGTTATCACTCATGGTTA
TGGCAGCACTGCATAATTCTCTTACTGTTCATGCCATCCGTAAGATGCT
TTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTA
TGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACC
GCGCCACATAGCAGAACTTTAAAGTGCTCATCATTGGAAAACGTTCT
TCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTTCG
ATGTAACCCACTCGTGCACCACTGATCTTCAGCATCTTTTACTTTCA
CCAGCGTTTTCTGGGTGAGCAAAAAACAGGAAGGCAAAATGCCGCAAAA
AAGGGAATAAGGGCGACACGAAATGTTGAATACTCATACTCTTCCT
TTTTCAATATATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGG
ATACATATTTGAATGTATTAGAAAAATAACAAATAGGGGTTCCGC
GCACATTTCCCCGAAAAGTGCCACCT

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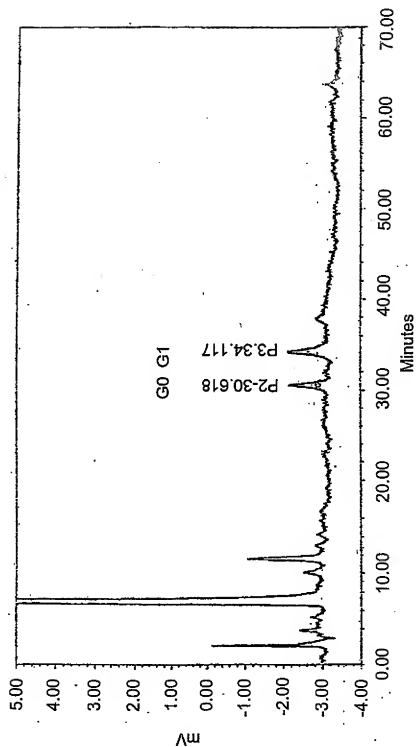


FIG. 97A.

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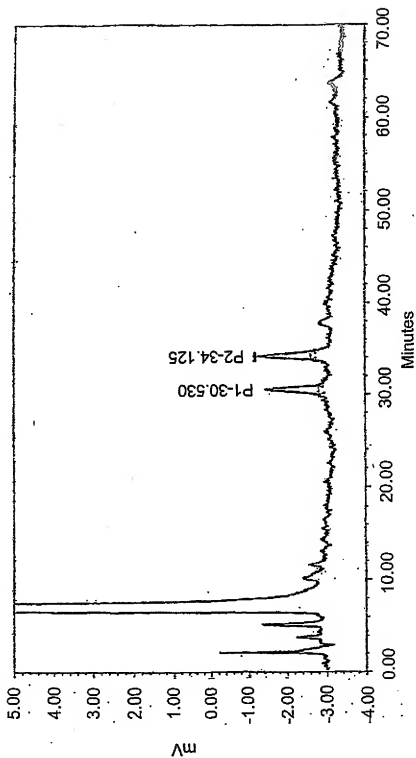


FIG. 97B

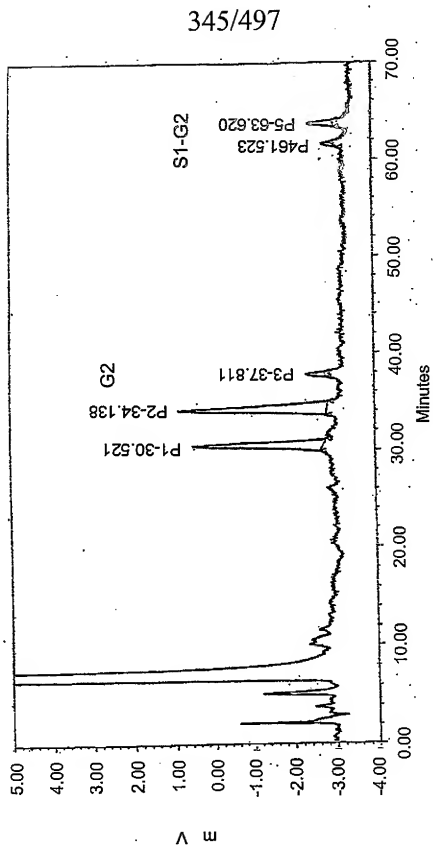


FIG. 97C

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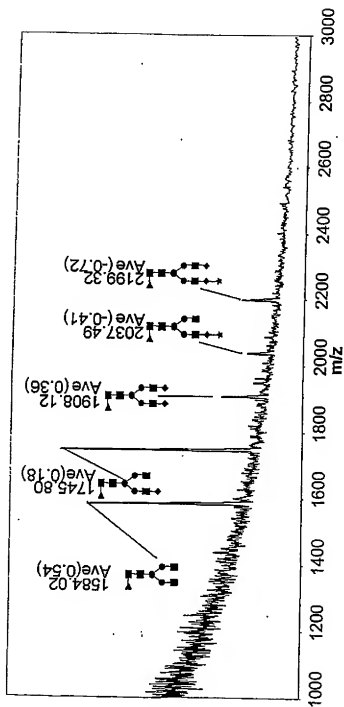


FIG. 98A

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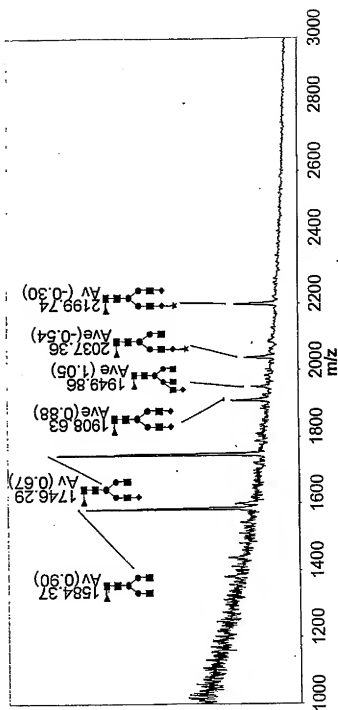


FIG. 98B

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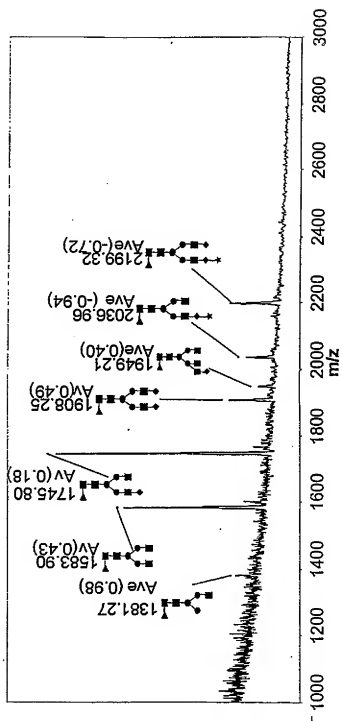


FIG. 98C

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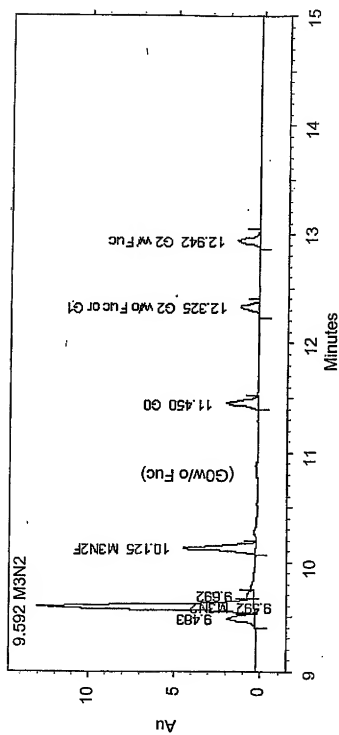


FIG. 99A

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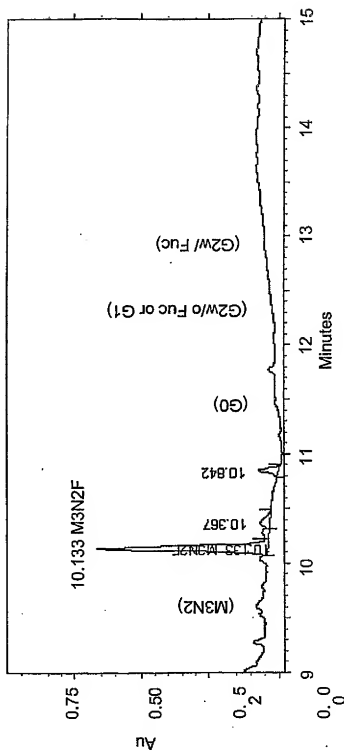


FIG. 99B

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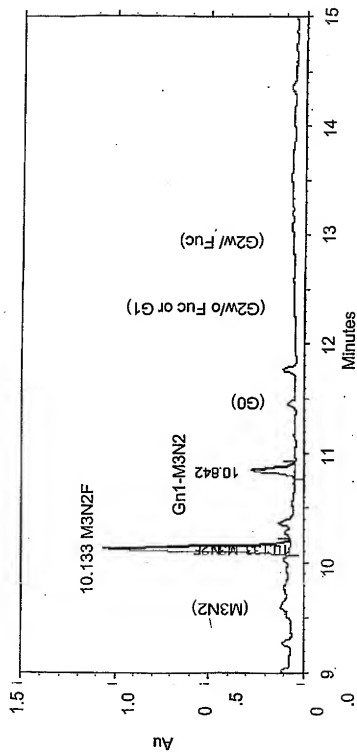


FIG. 99C

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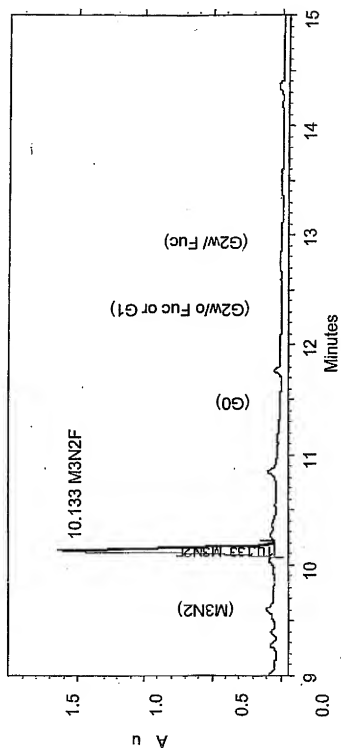


FIG. 99D

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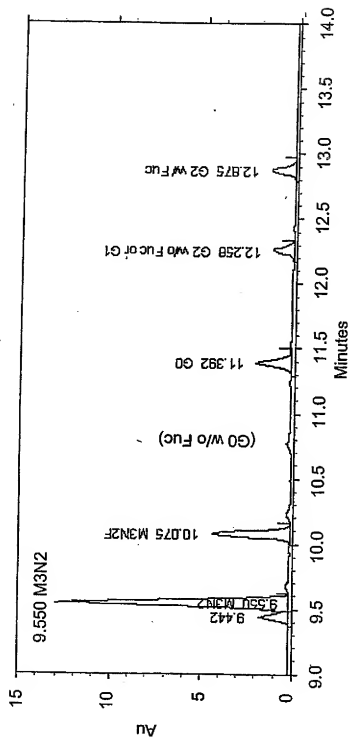


FIG. 100A

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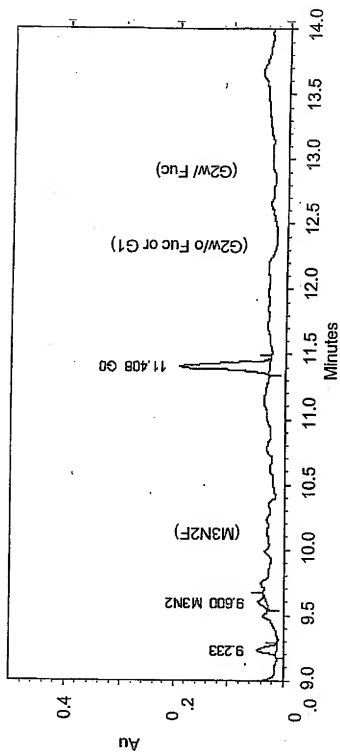


FIG. 100B

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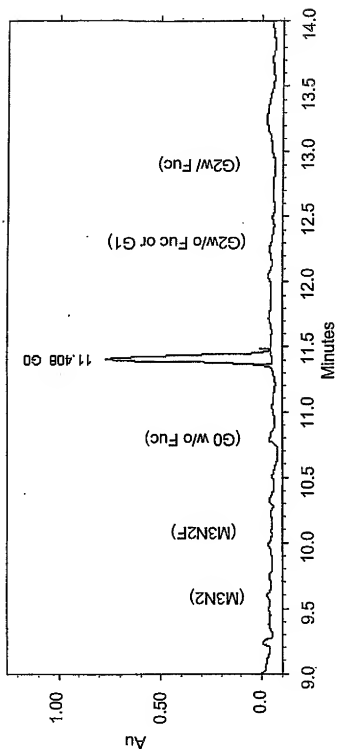


FIG. 100D

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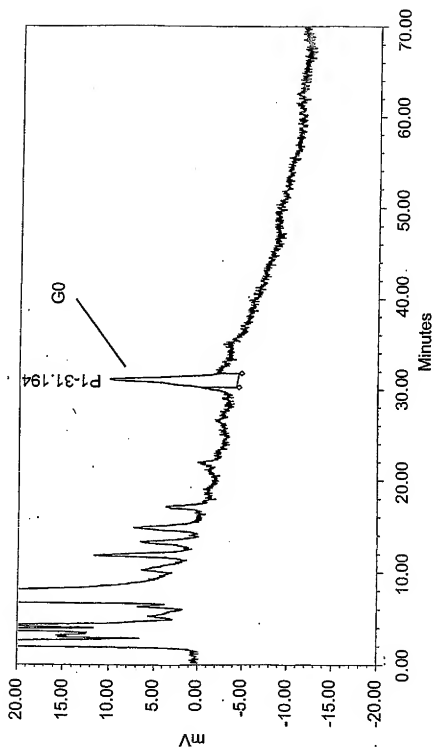


FIG. 101A

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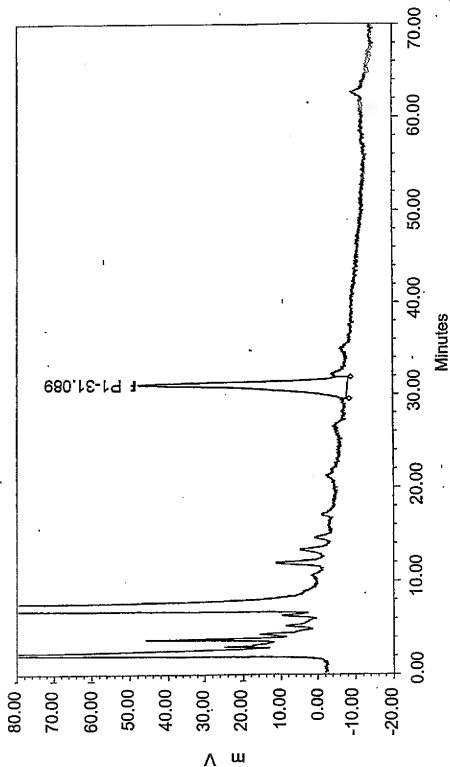


FIG. 101B

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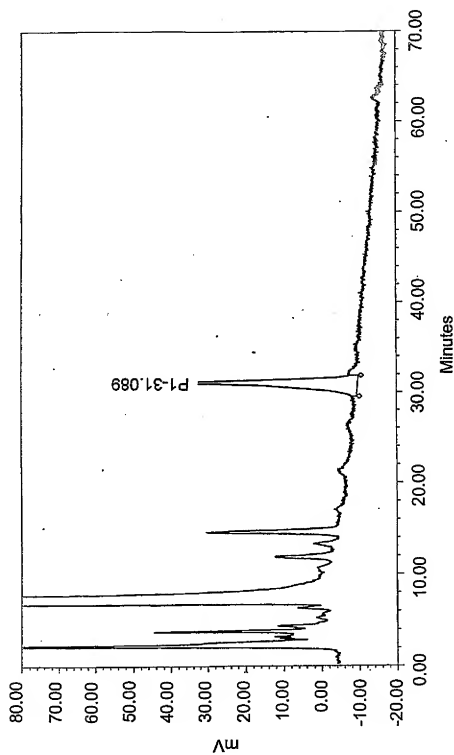


FIG. 101C

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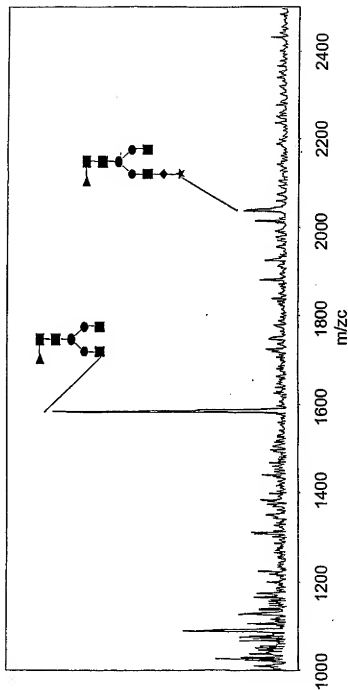
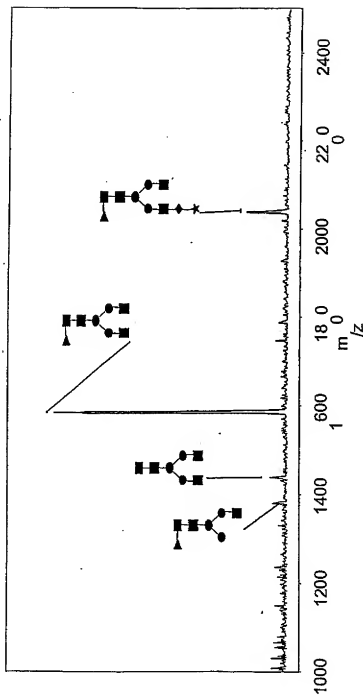


FIG. 102A

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FIG. 10^B

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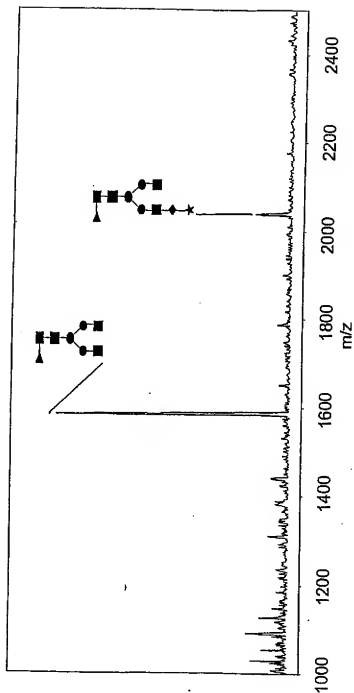


FIG. 102C

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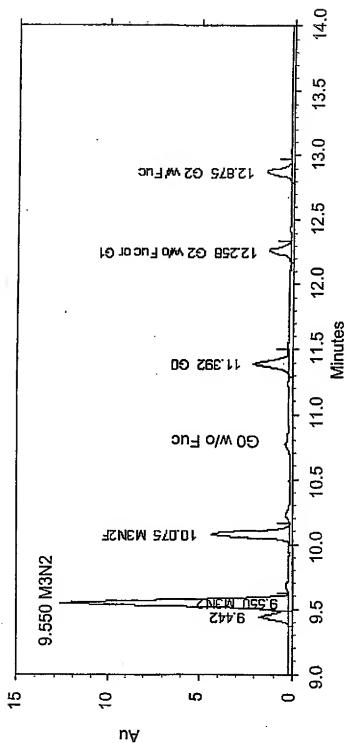


FIG. 103A

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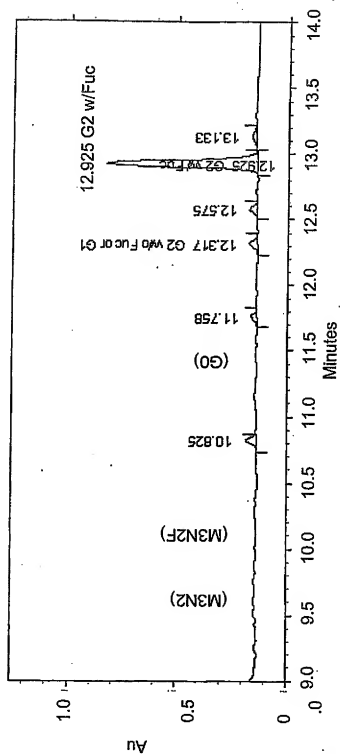


FIG. 103B

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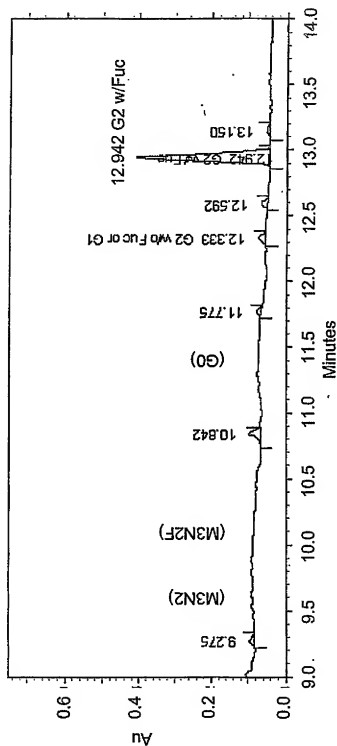


FIG. 103C

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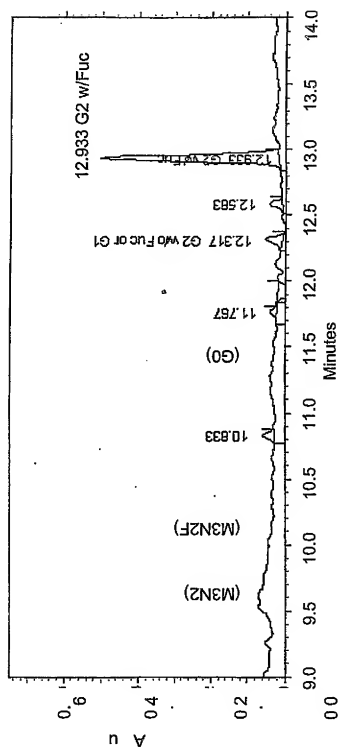


FIG. 103D

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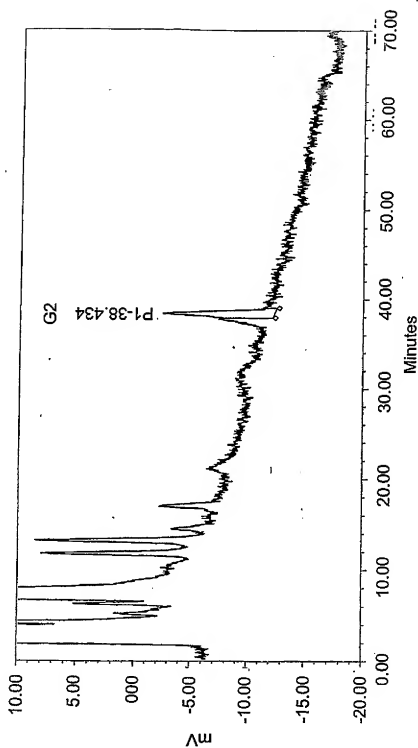


FIG. 104A

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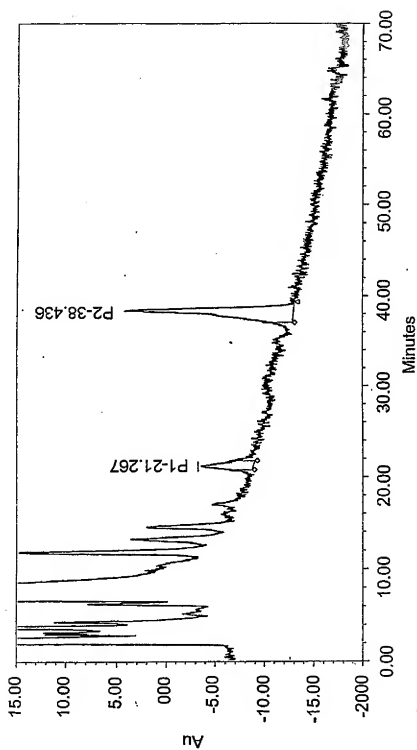


FIG. 104B

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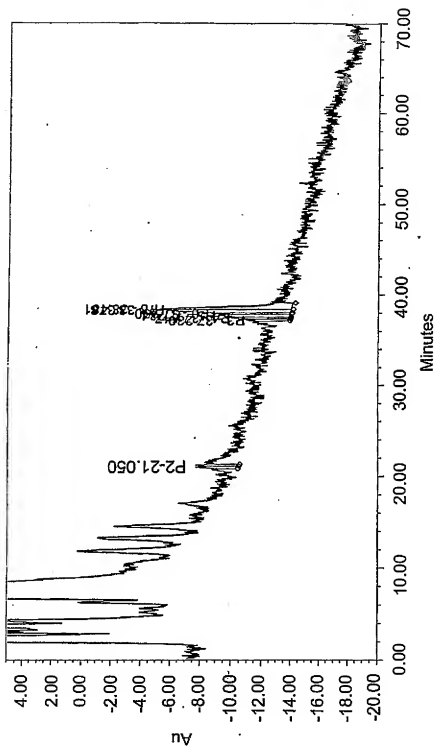


FIG. 104C

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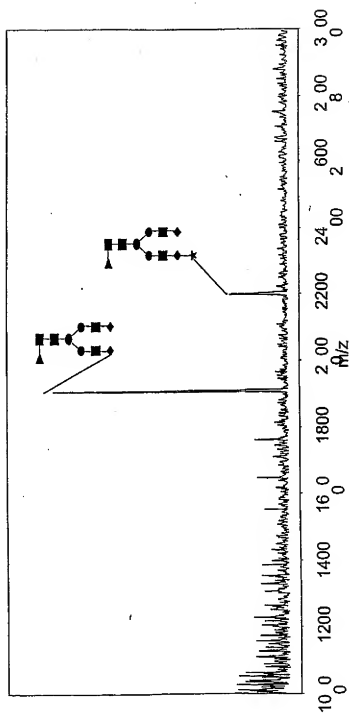


FIG. 105A

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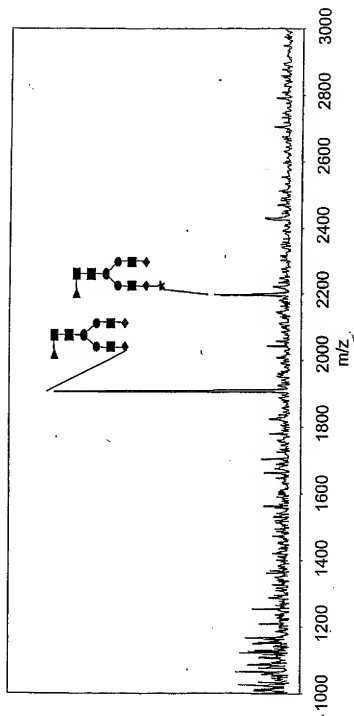


FIG. 105B

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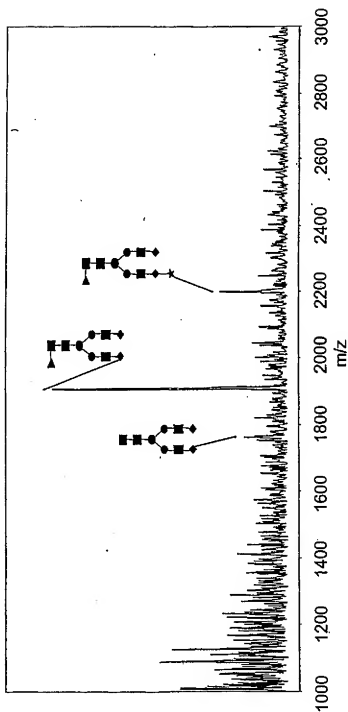


FIG. 105C

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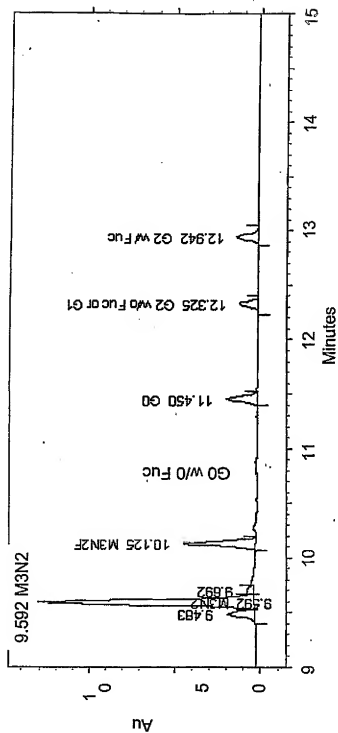


FIG. 106A

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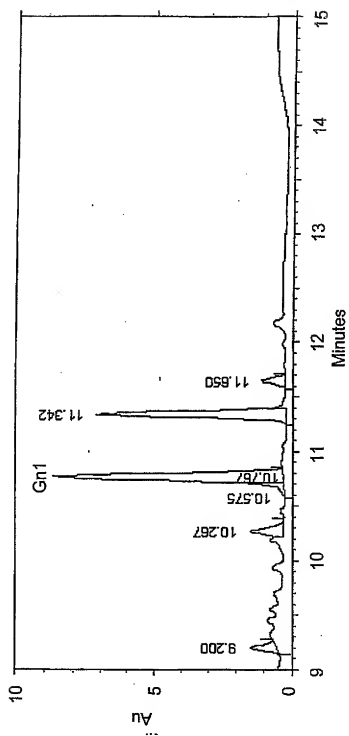


FIG. 106B

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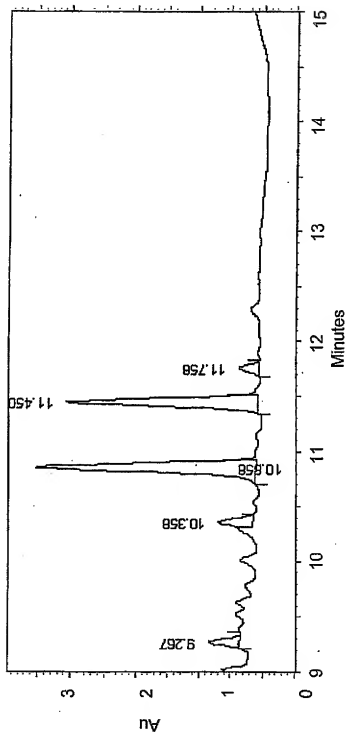


FIG. 106C

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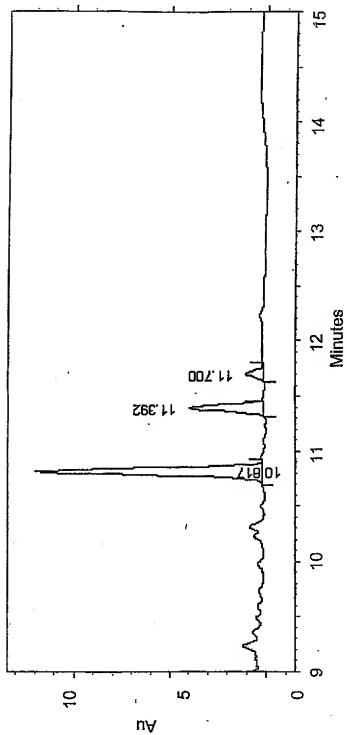


FIG. 106D

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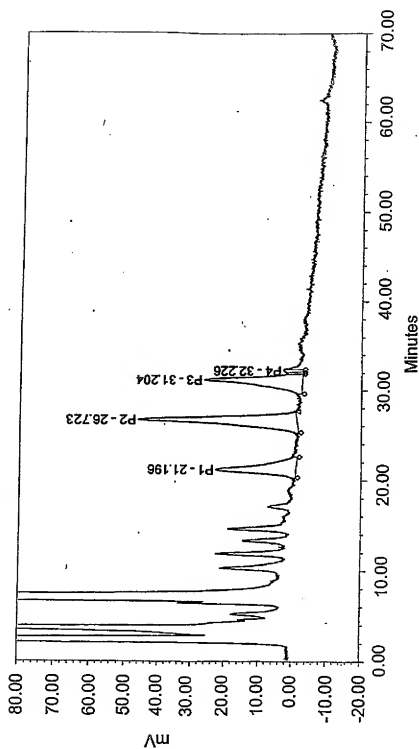


FIG. 107A

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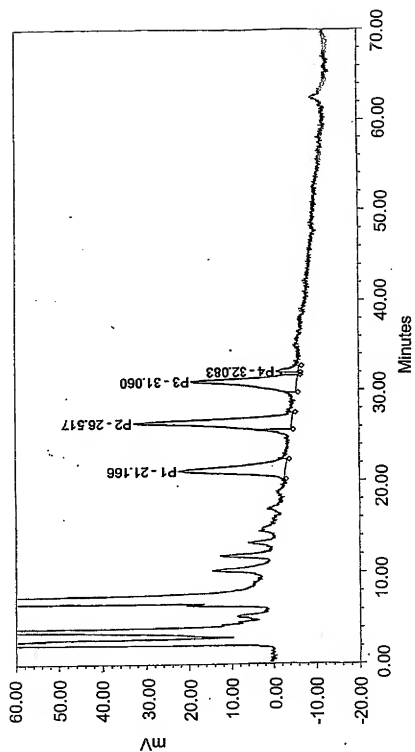


FIG. 107B

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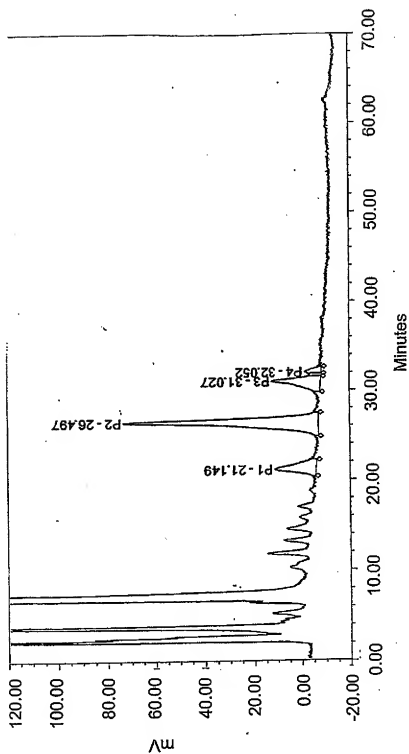


FIG. 107C

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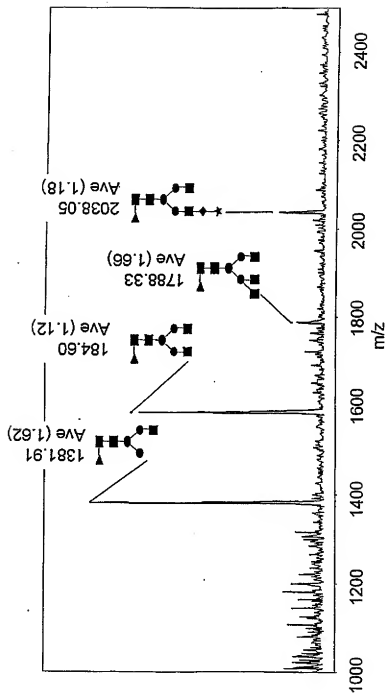
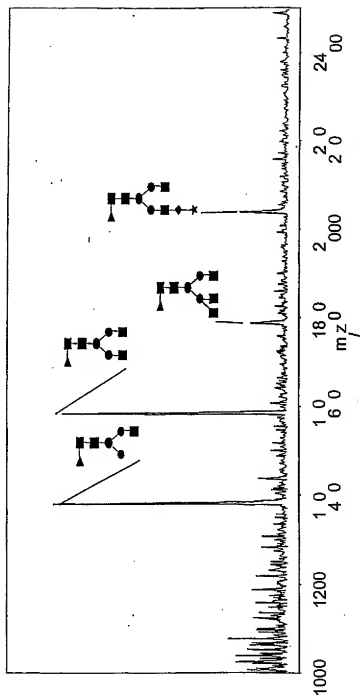


FIG. 108A

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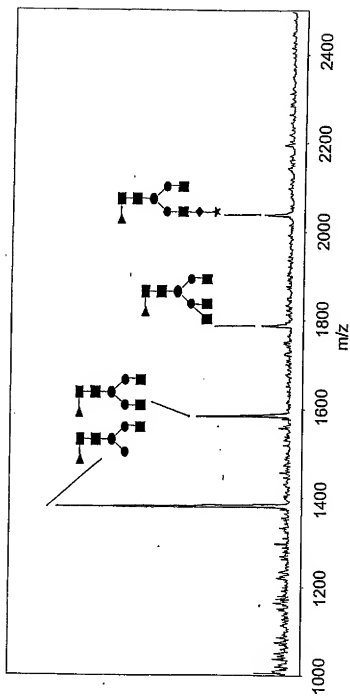


FIG. 108C

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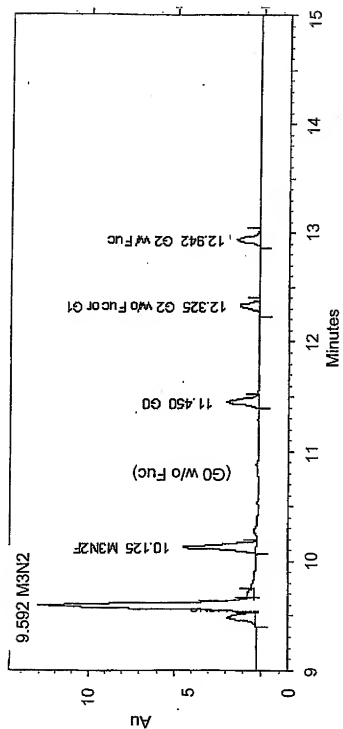


FIG. 109A

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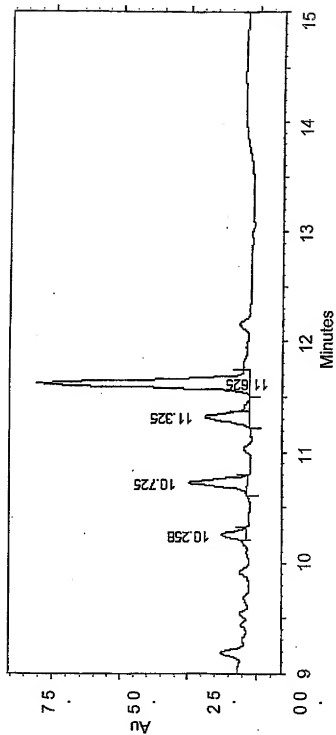


FIG. 109B

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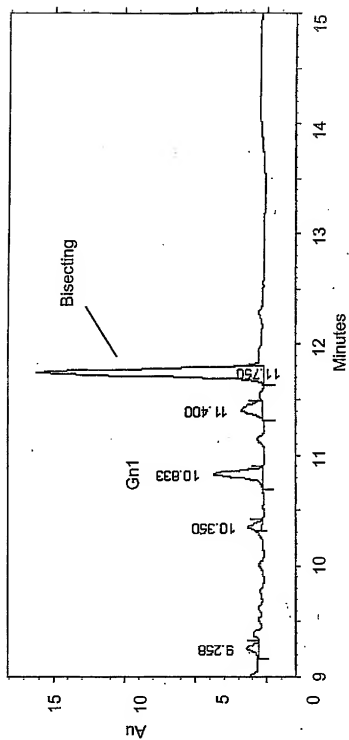


FIG. 109C

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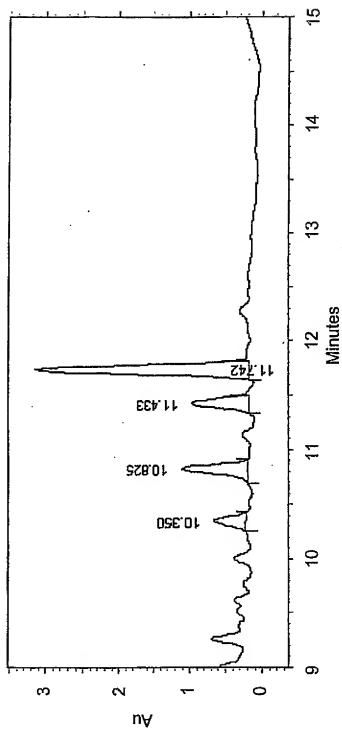


FIG. 109D

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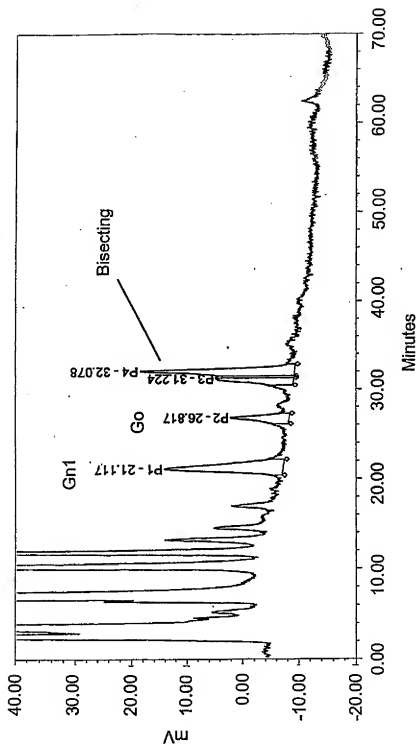


FIG. 110A

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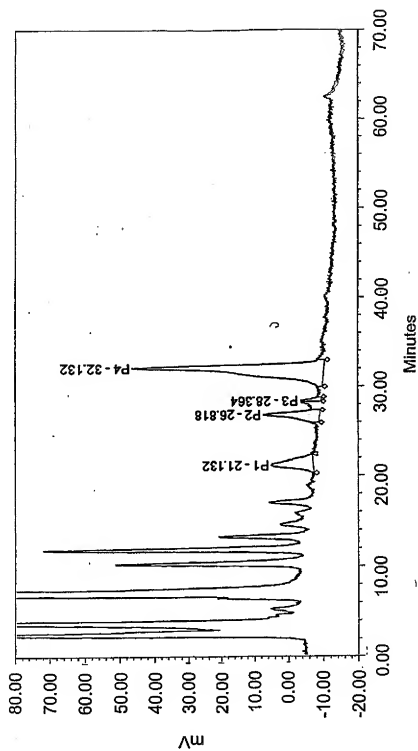


FIG. 110B

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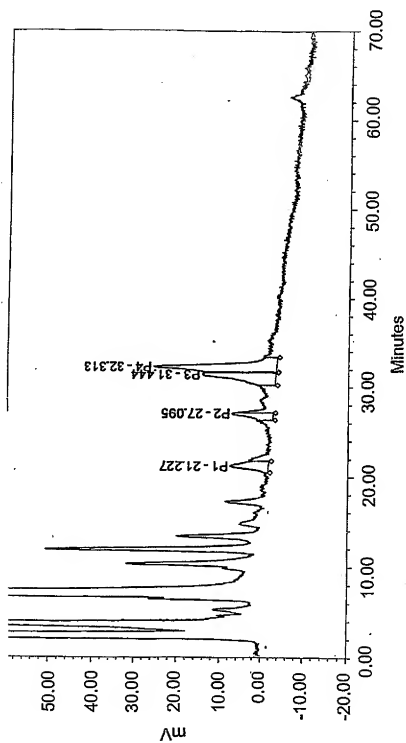


FIG. 110C

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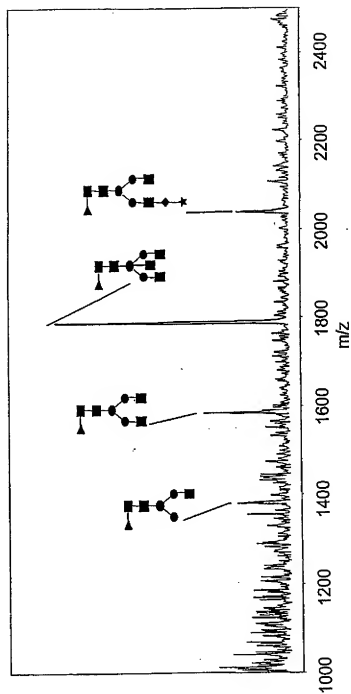


FIG. 111A

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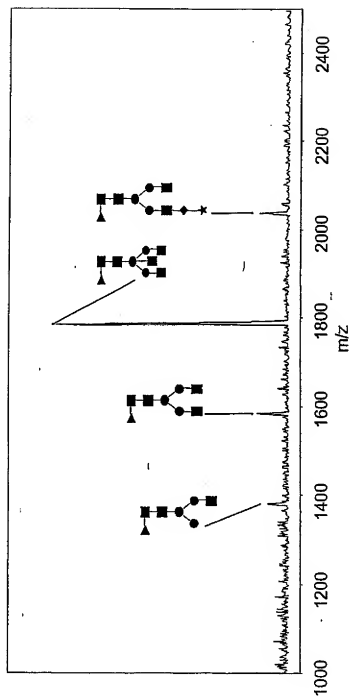


FIG. 111B

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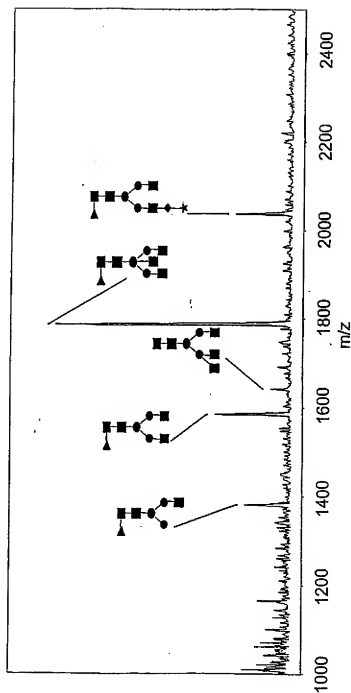


FIG. 111C

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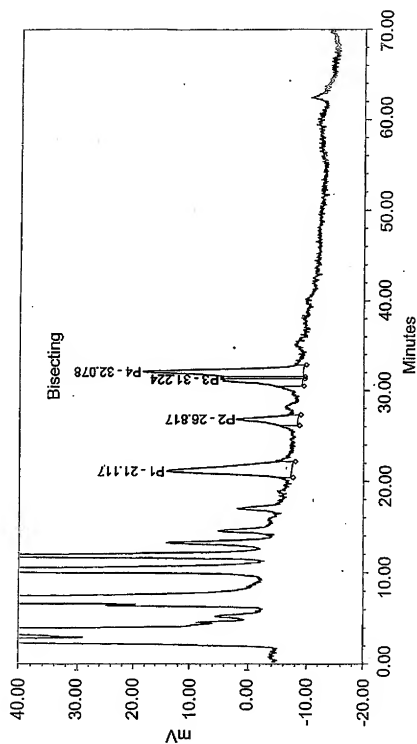


FIG. 112A

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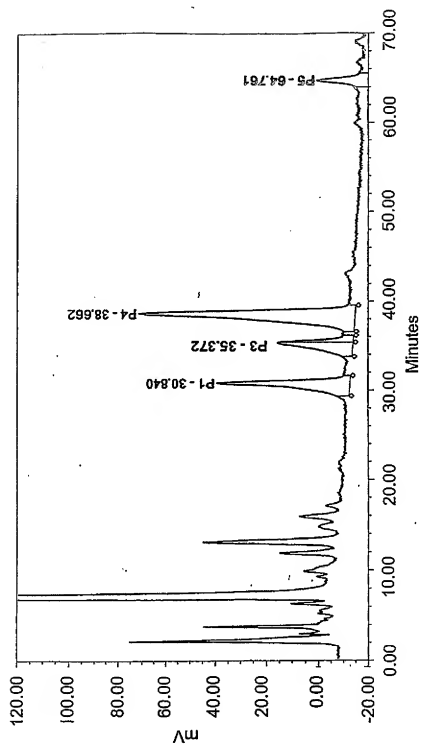


FIG. 112B

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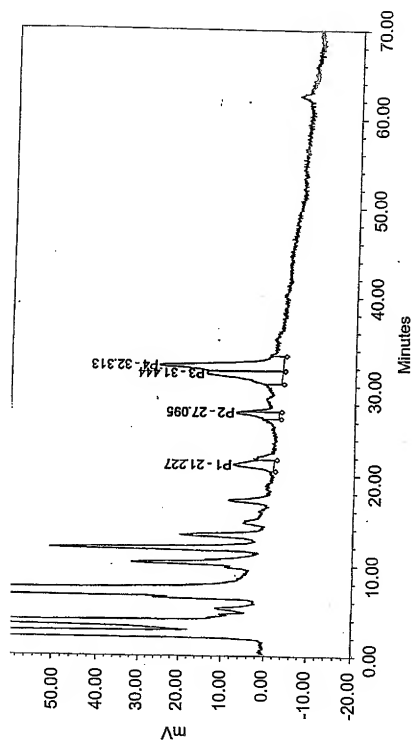


FIG. 112C

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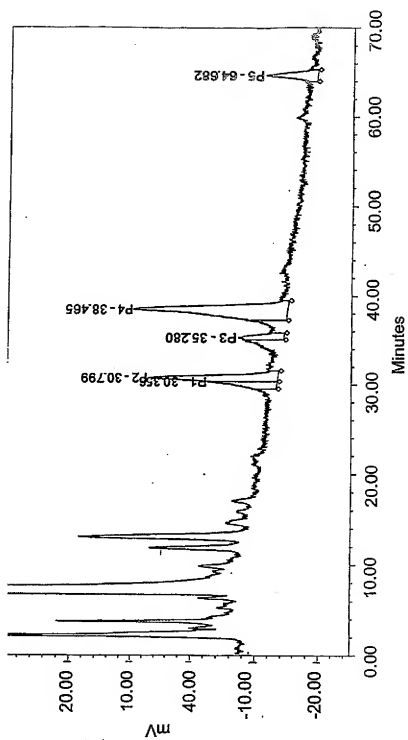


FIG. 112D

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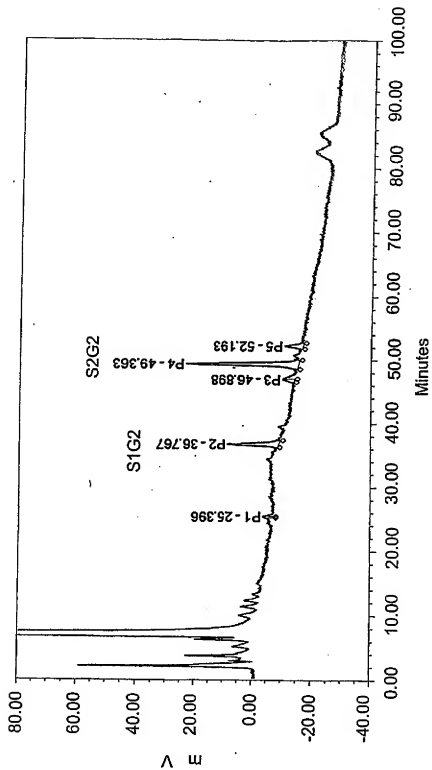


FIG. 113A

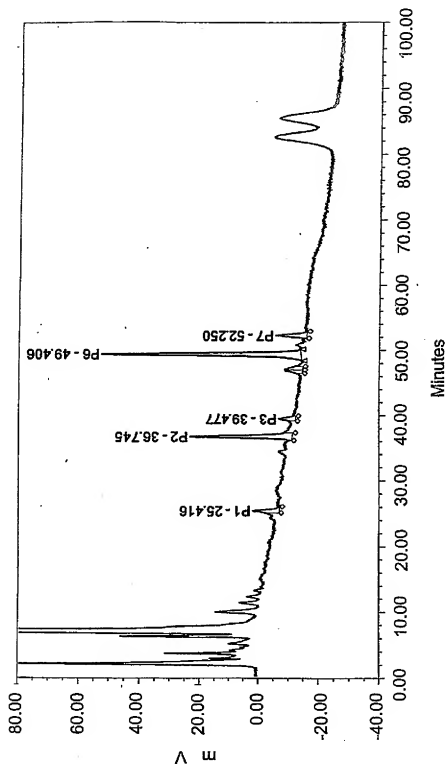


FIG. 113B

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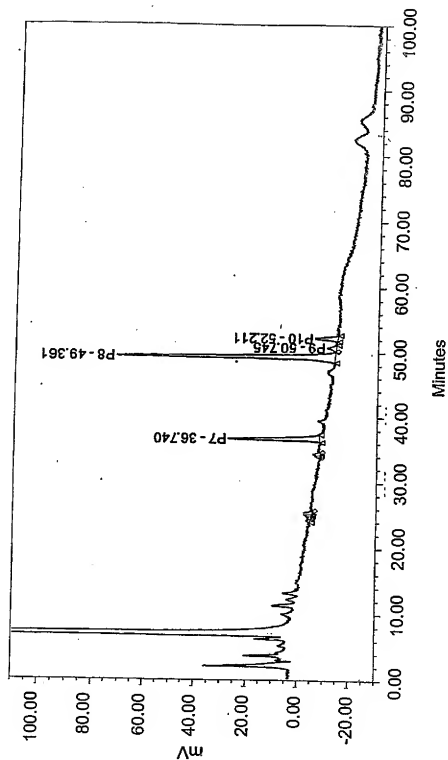


FIG. 113C

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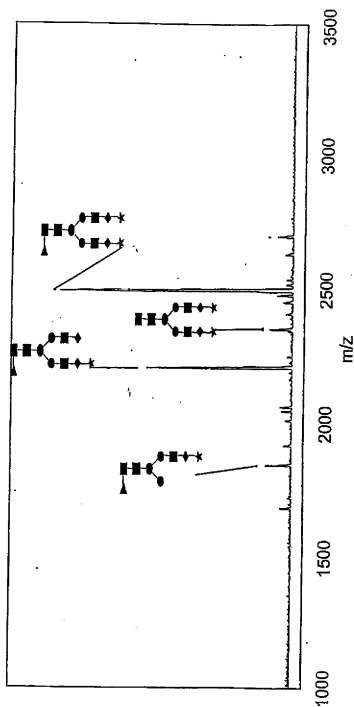
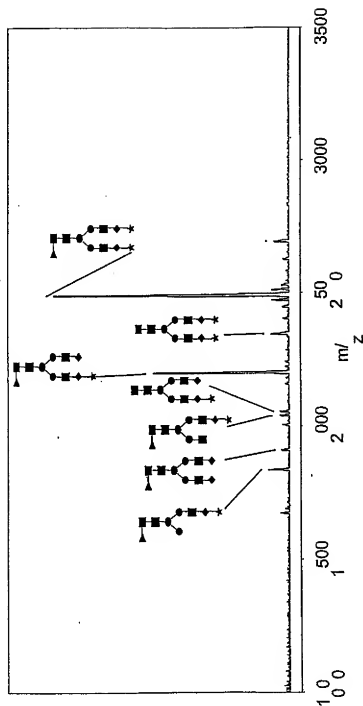
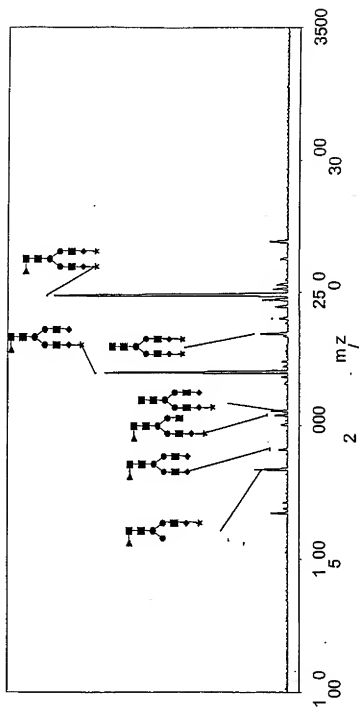


FIG. 114A

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FIG. 1₄B

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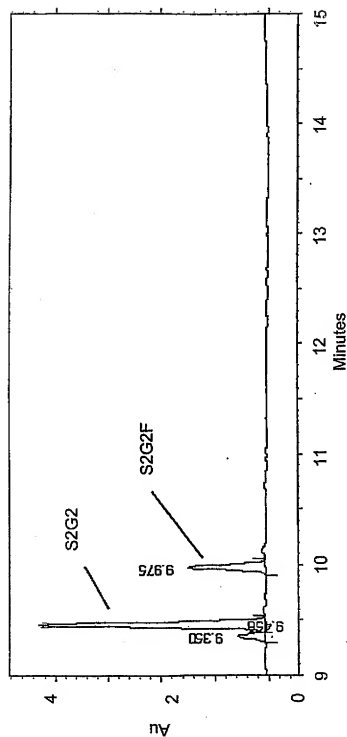


FIG. 115A

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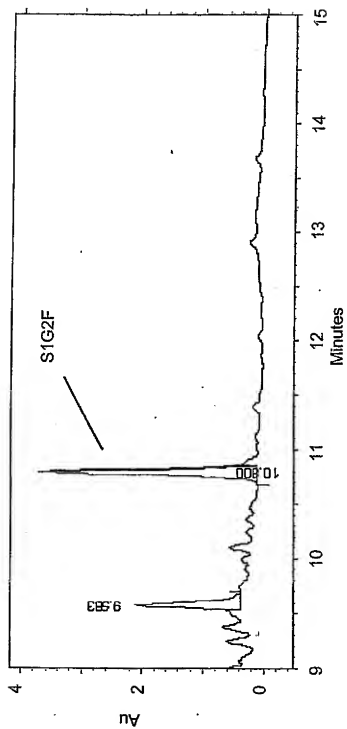


FIG. 115B

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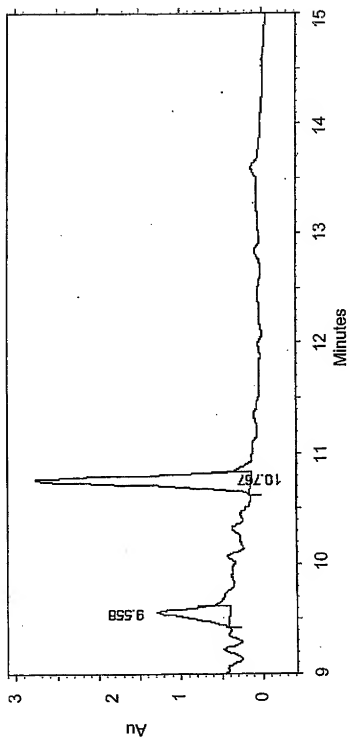


FIG. 115C

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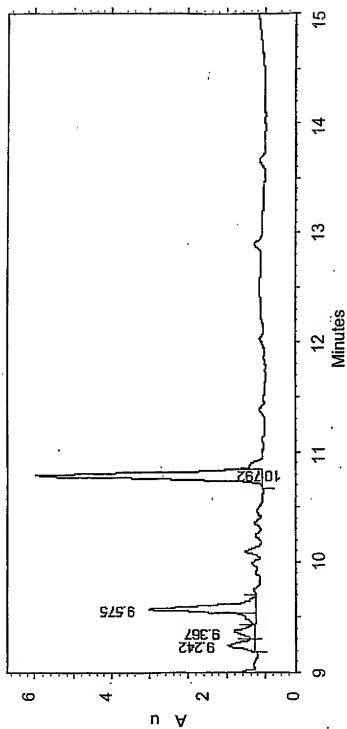


FIG. 115D

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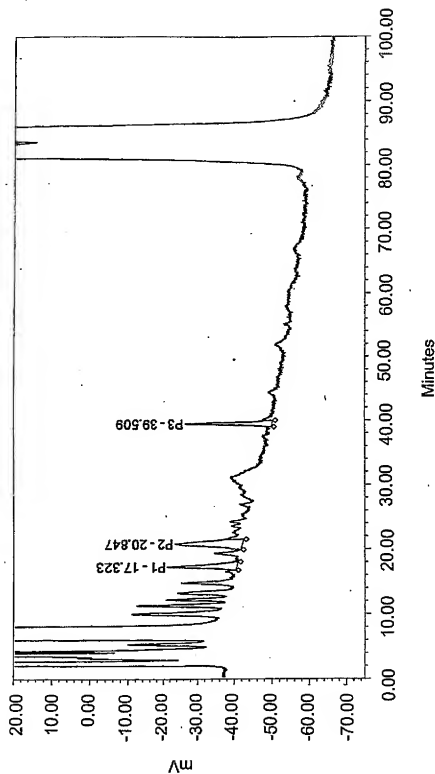


FIG. 116A

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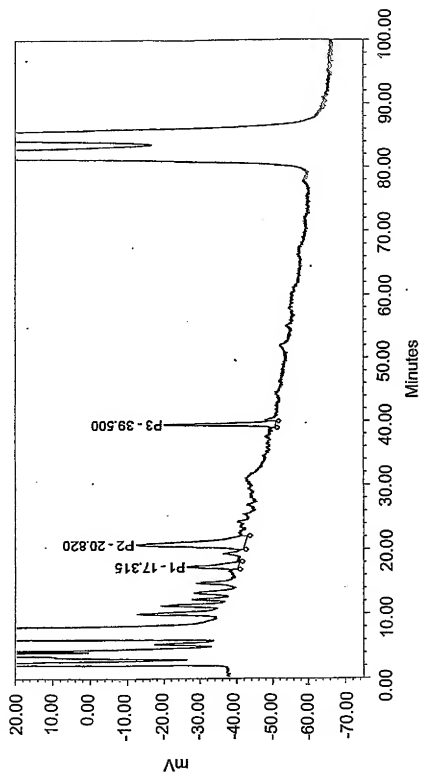


FIG. 116B

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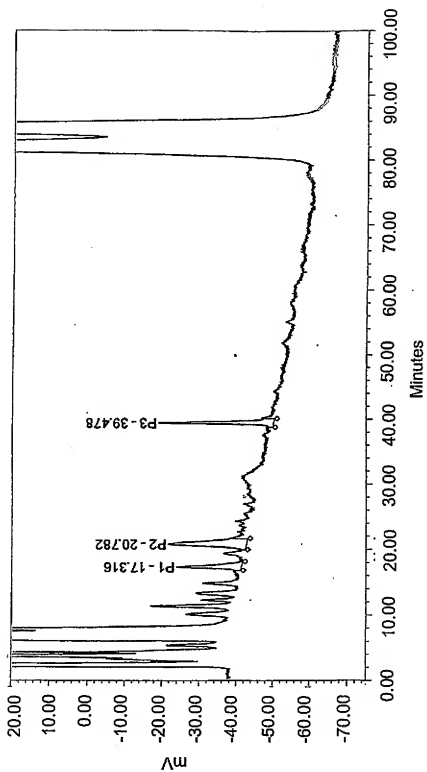


FIG. 116C

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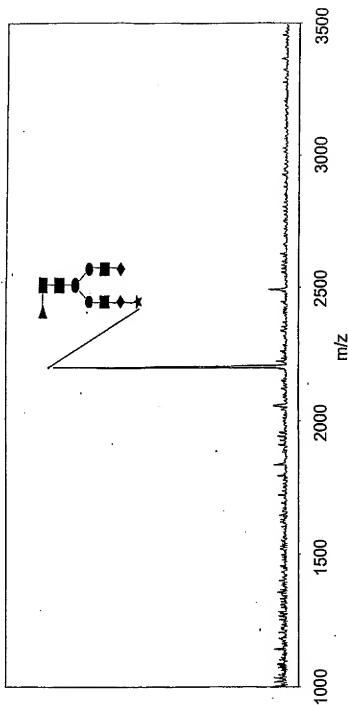


FIG. 117A

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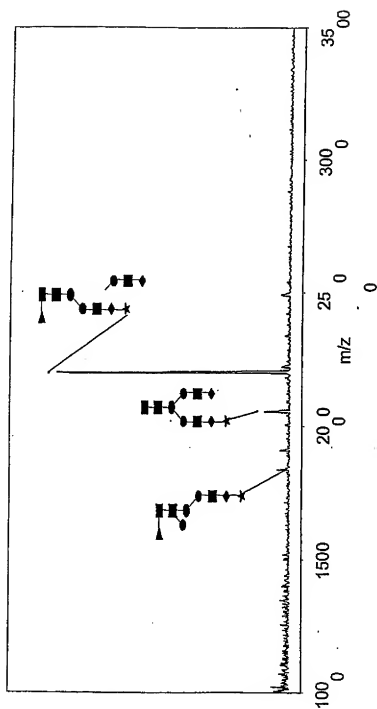


FIG. 17B

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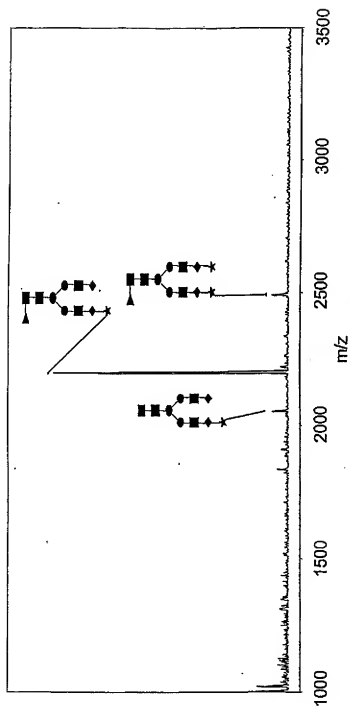


FIG. 117C

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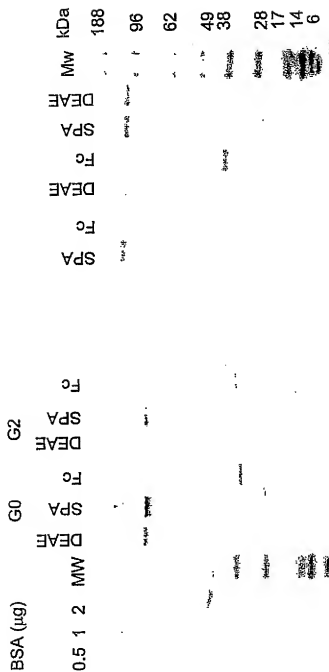


FIG. 118B

FIG. 118A

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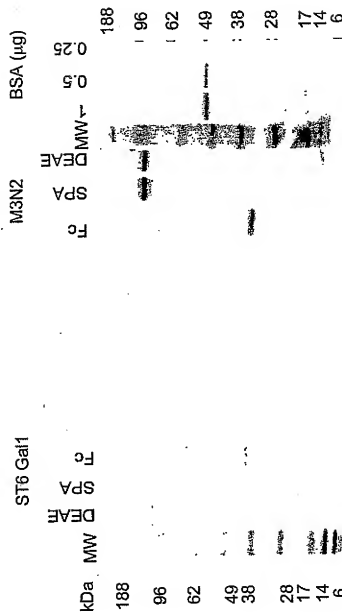


FIG. 118D

FIG. 118C

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BSA (μ g)	Gal-bisecting
0	DEAE
2	Fc
5	SPA
1	

-1850

-1850

-1850

-1850

-1850

FIG 118E

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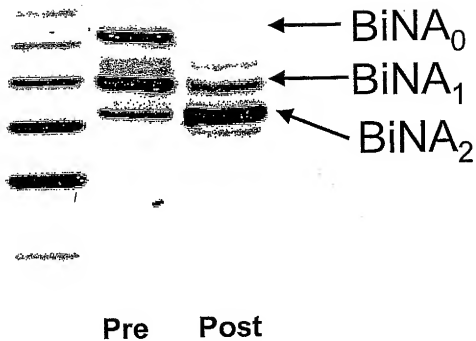


FIG. 119

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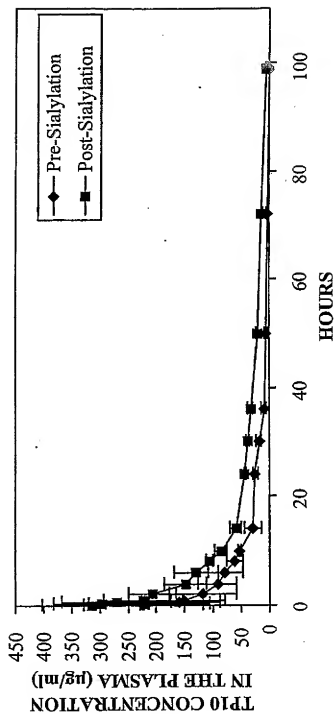


FIG. 120

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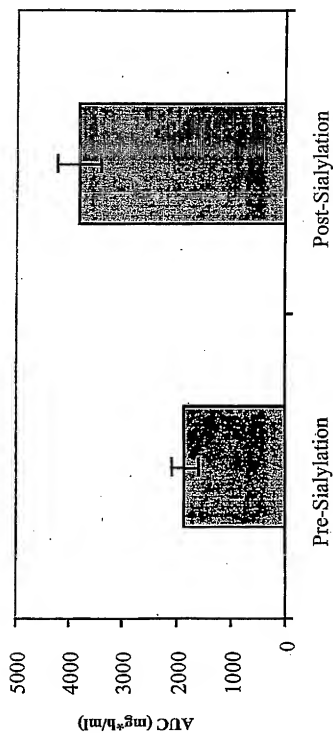


FIG. 121

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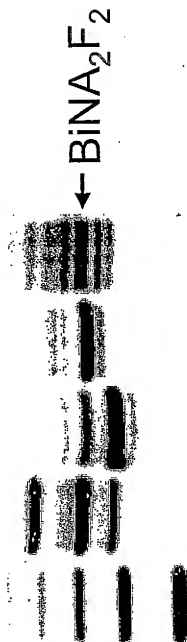


FIG. 122

Pre +SA +F TP20

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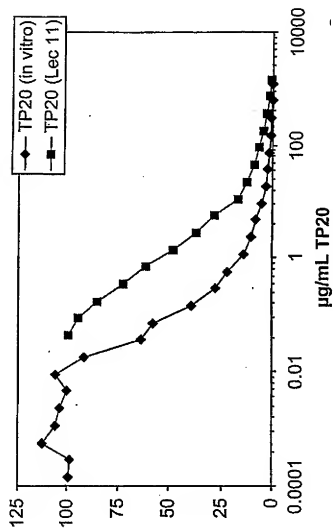


FIG. 123

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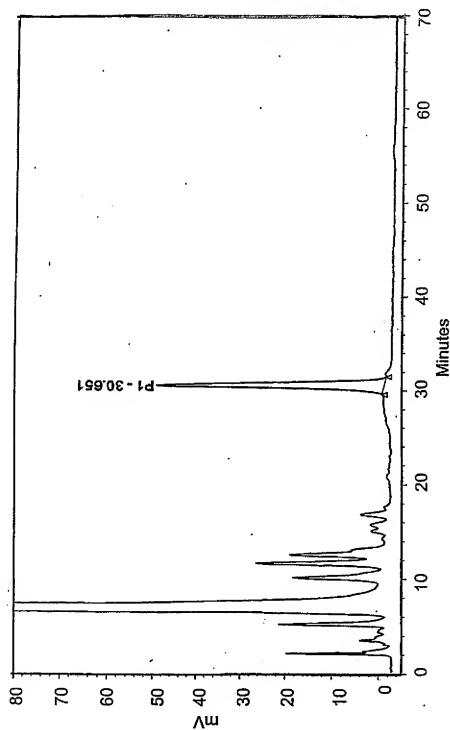


FIG. 124

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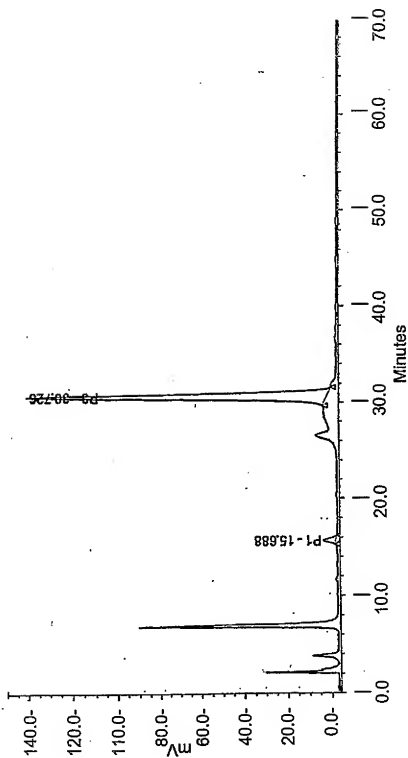


FIG. 125A

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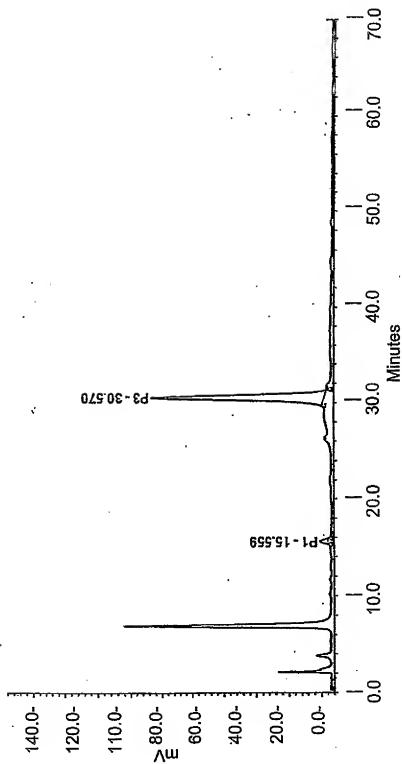


FIG. 125B

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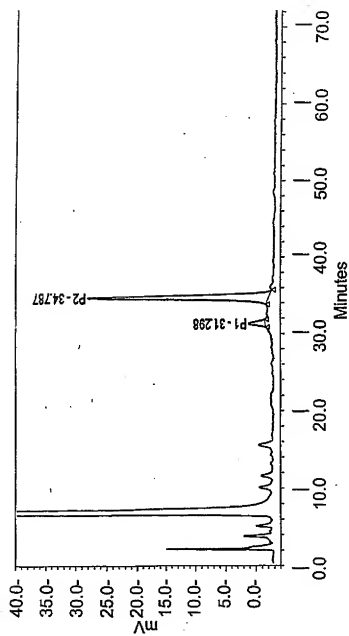
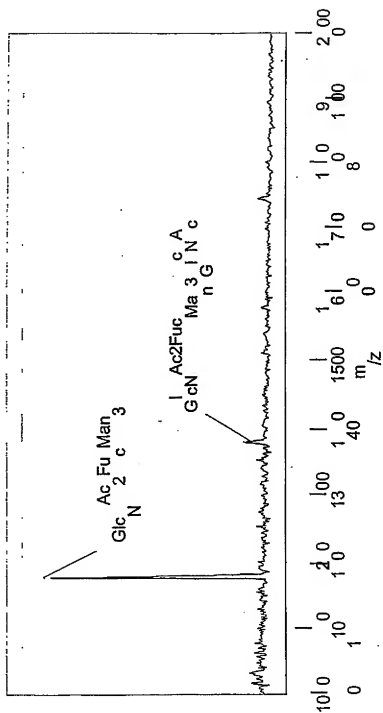


FIG. 126

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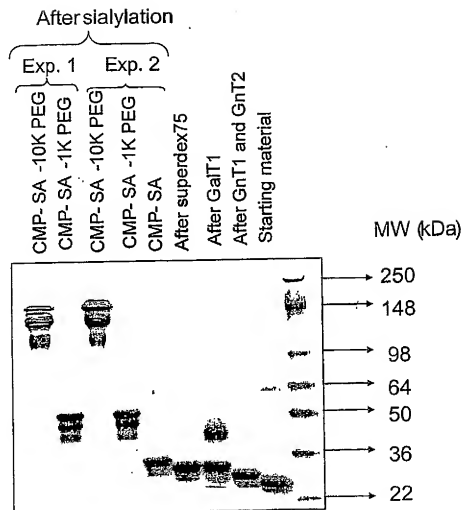
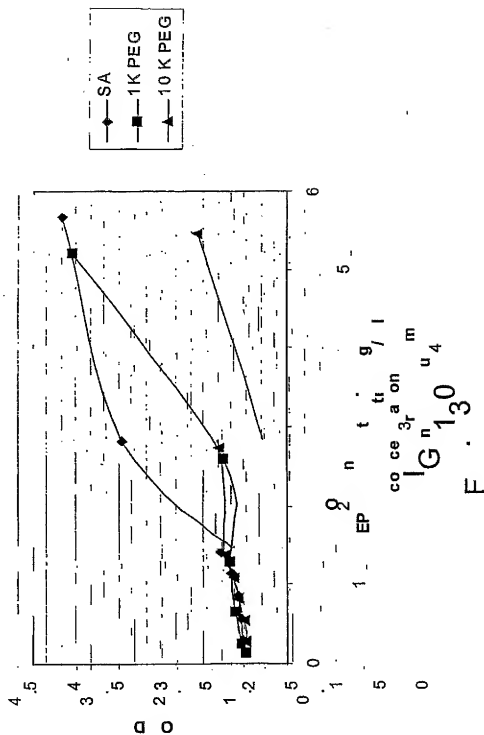
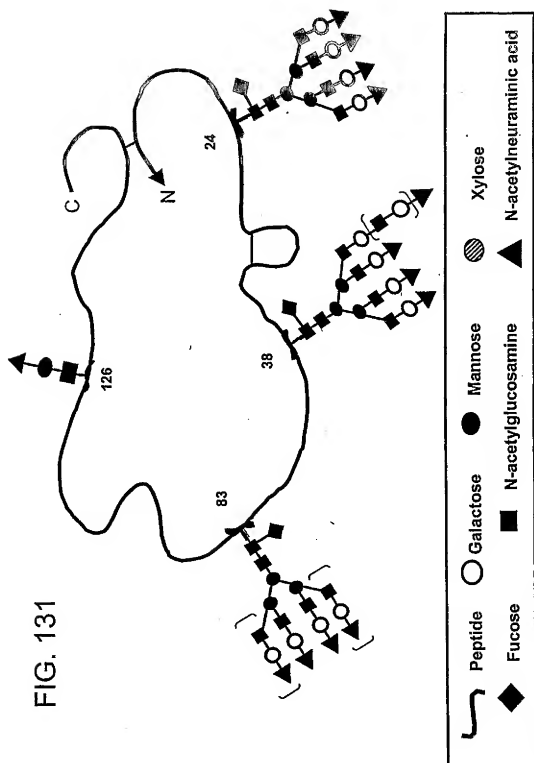


FIG. 129

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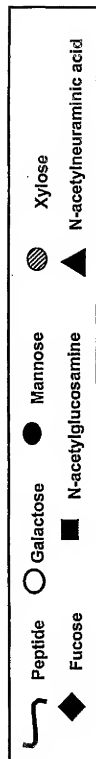
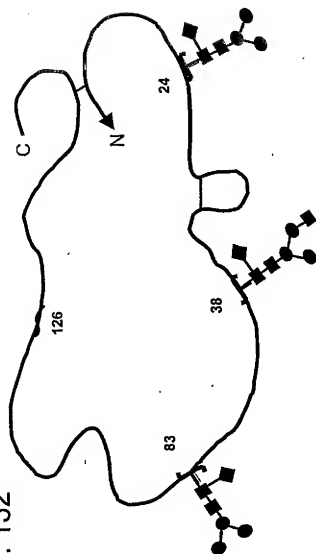


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FIG. 132



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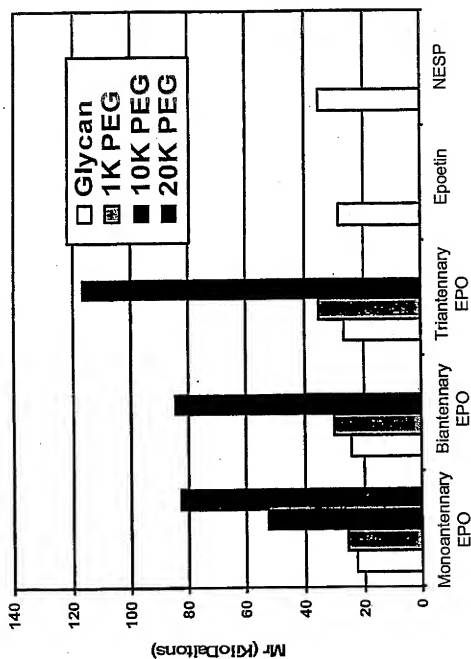
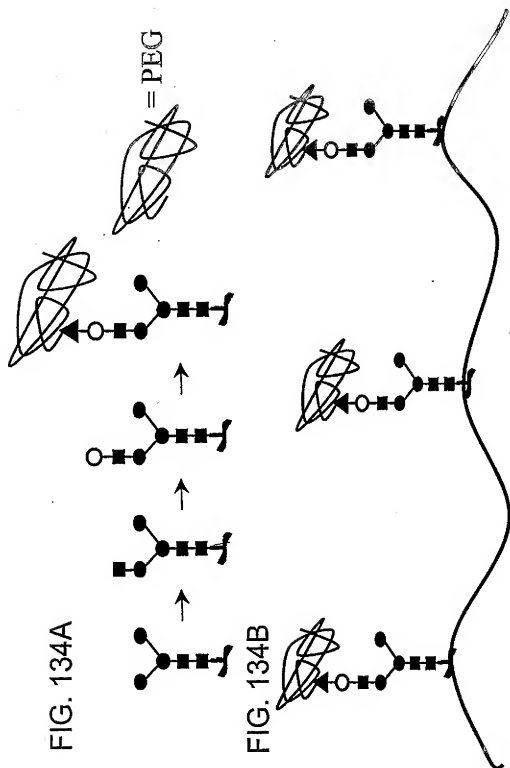


FIG. 133

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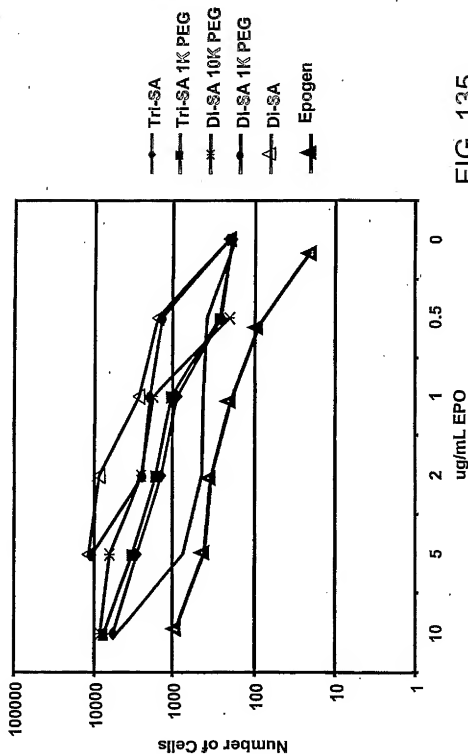


FIG. 135

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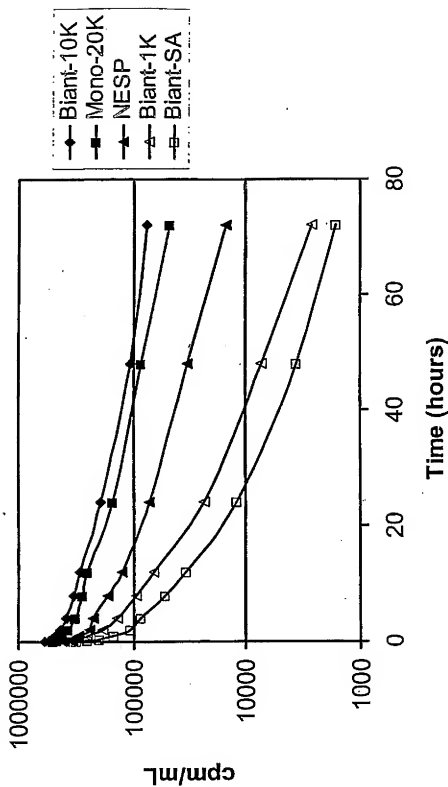


FIG. 136

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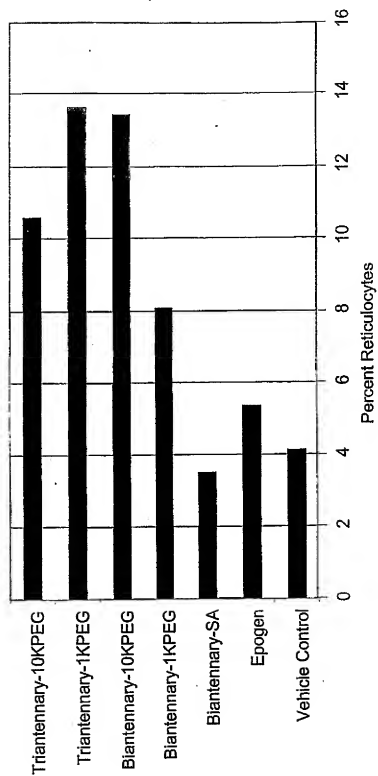


FIG. 137

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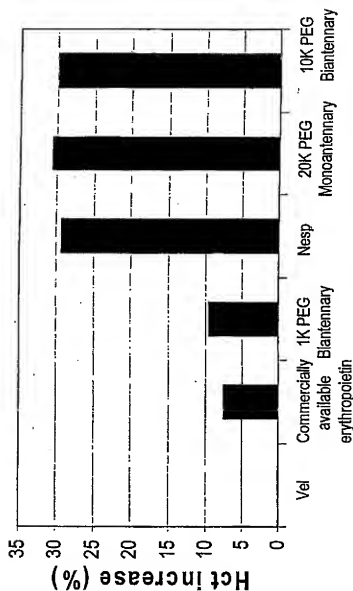


FIG. 138

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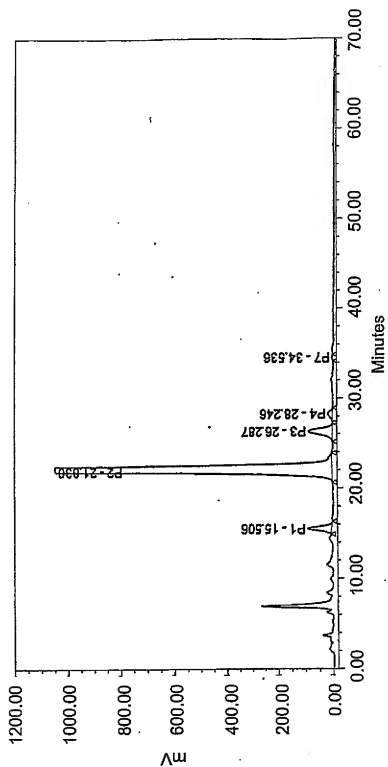


FIG. 139A

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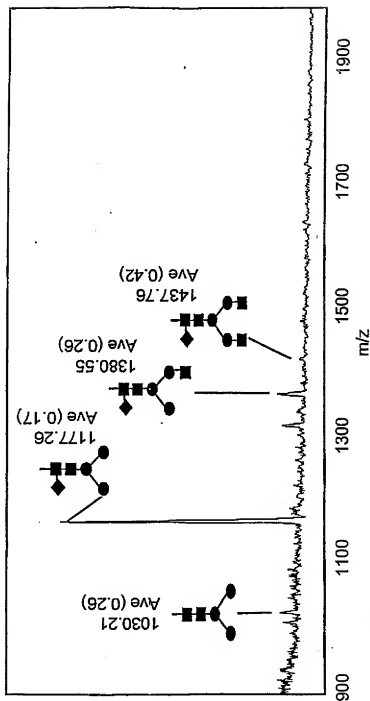


FIG. 139B

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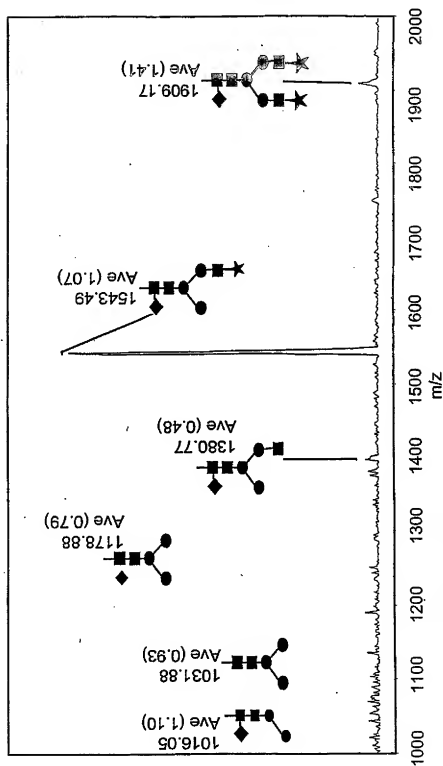


FIG. 140

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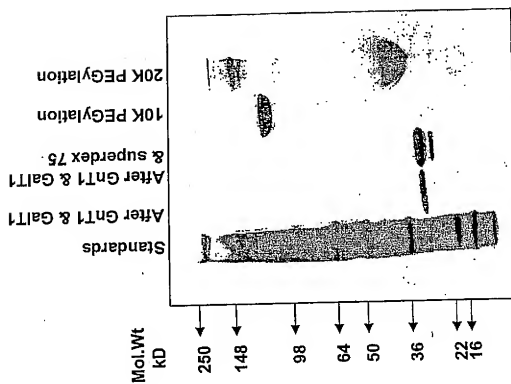


FIG. 141

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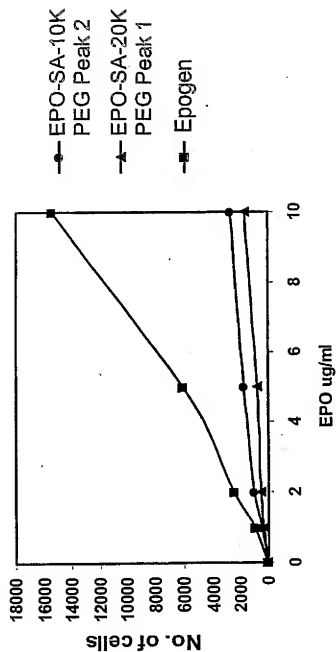


FIG. 142

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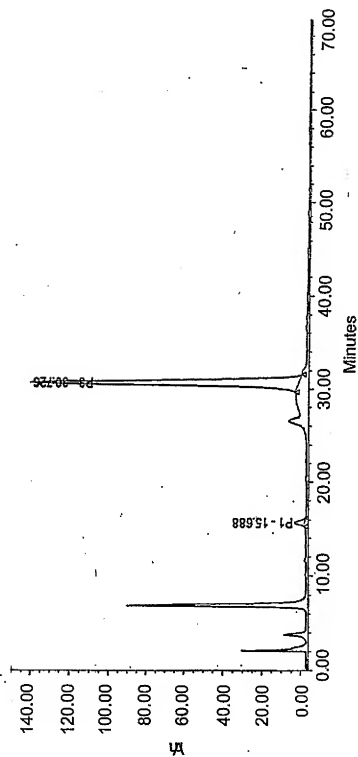


FIG. 143A

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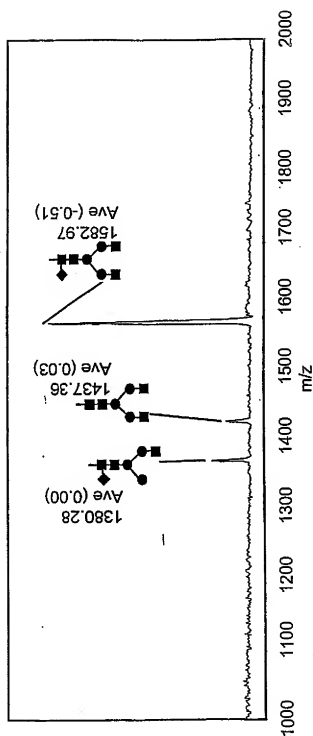


FIG. 143B

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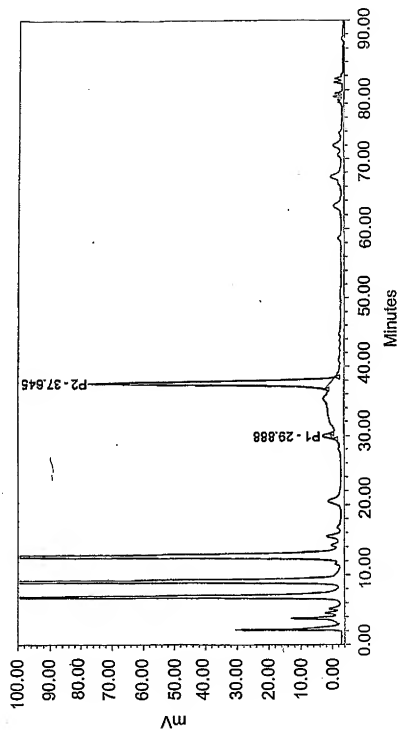


FIG. 144A

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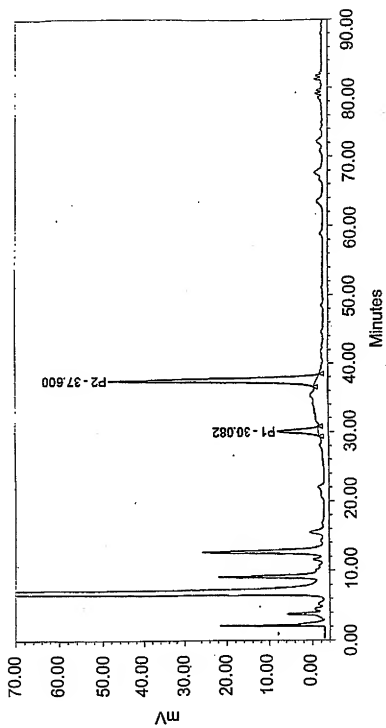


FIG. 144B

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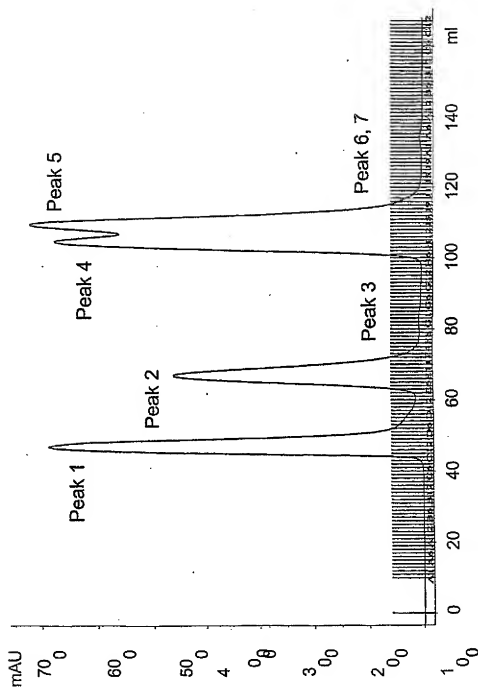


FIG. 145

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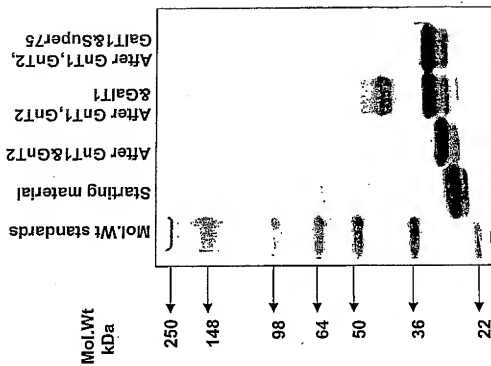
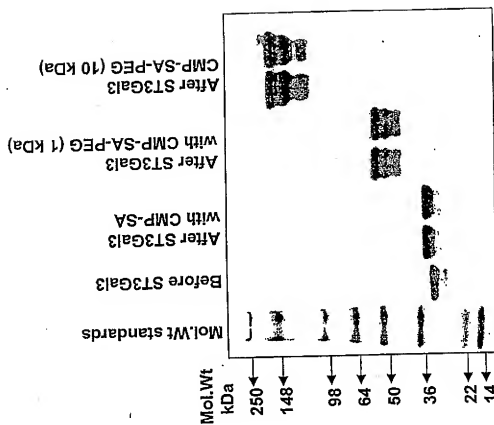


FIG. 146

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F₁G 147

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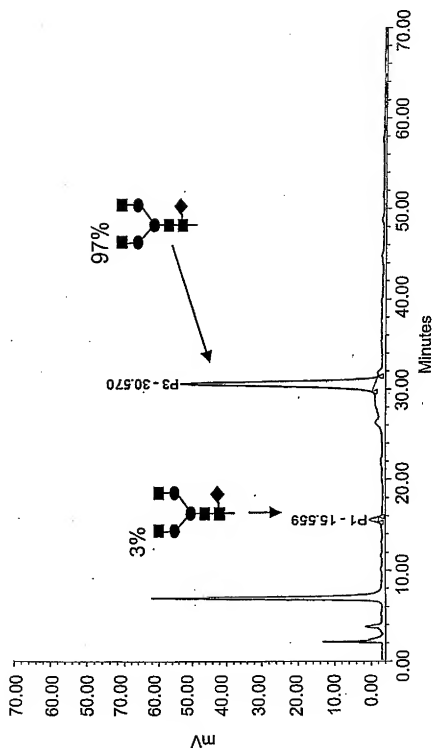


FIG. 148

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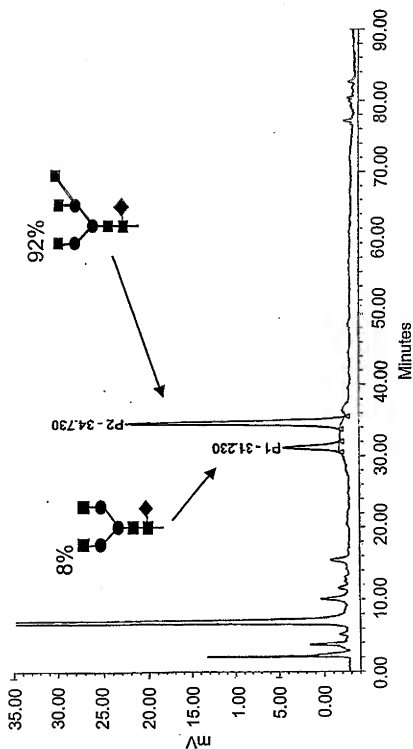


FIG. 149

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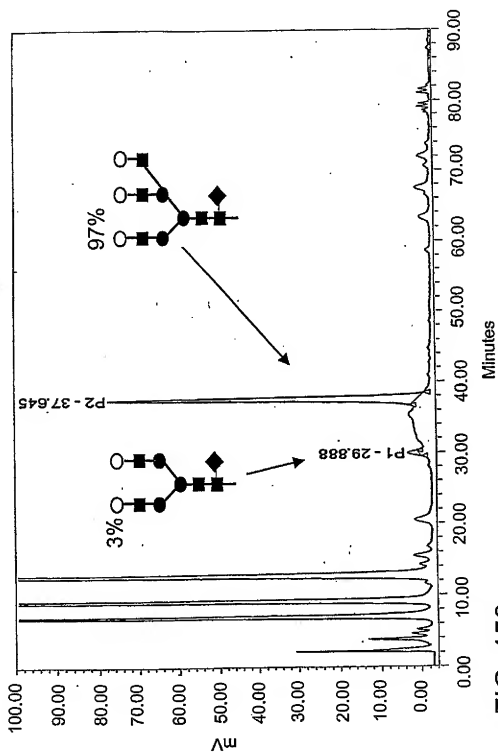


FIG. 150

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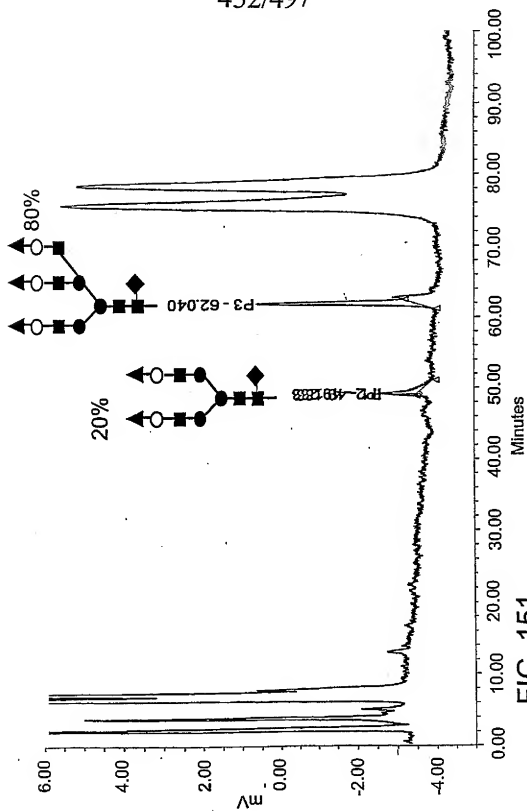


FIG. 151

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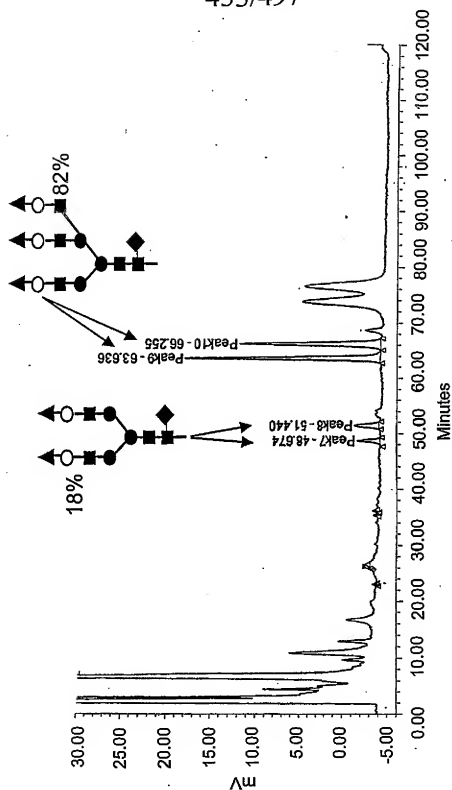


FIG. 152

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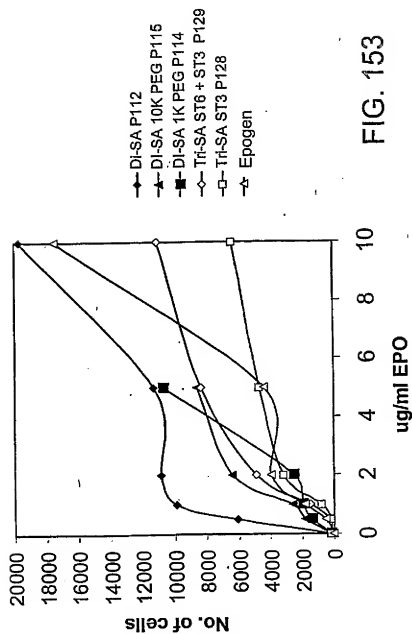


FIG. 153

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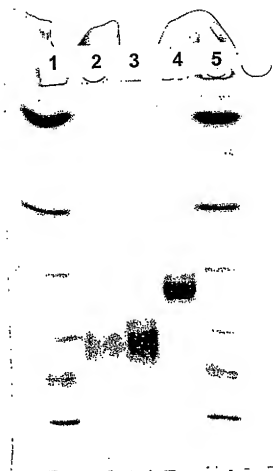


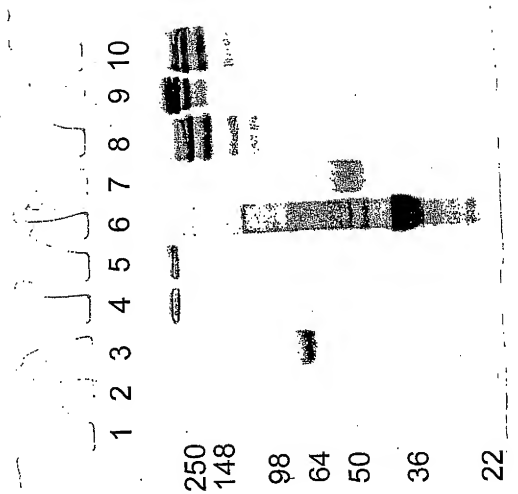
FIG. 154

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FIG. 155

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FIG 15₆

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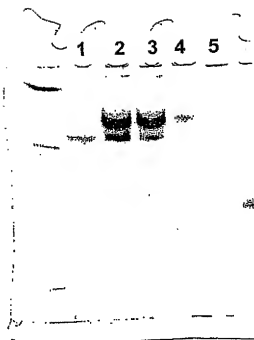


FIG. 157

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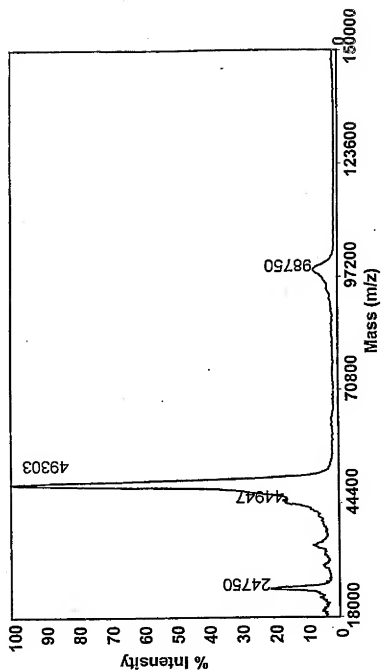


FIG. 158

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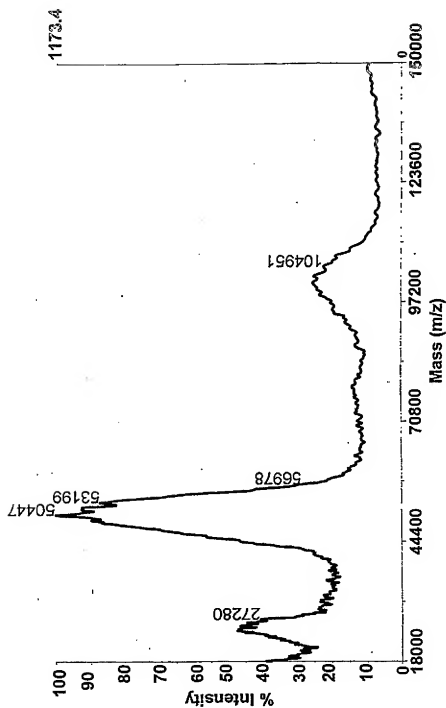


FIG. 159

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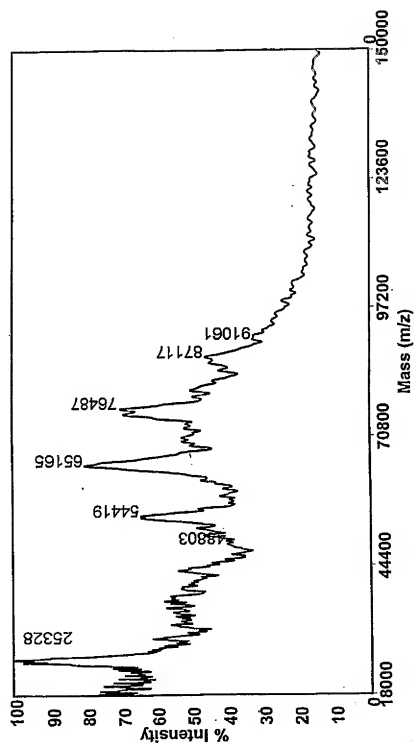


FIG. 160

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FIG. 161

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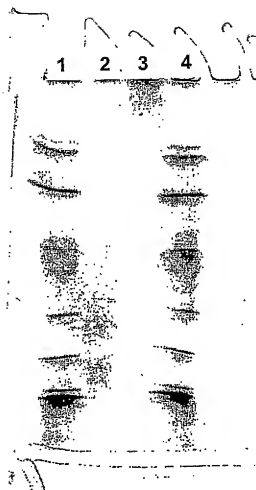


FIG. 162

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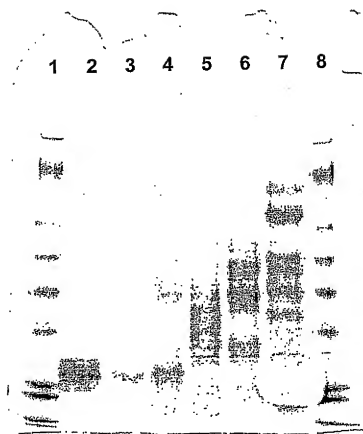


FIG. 163

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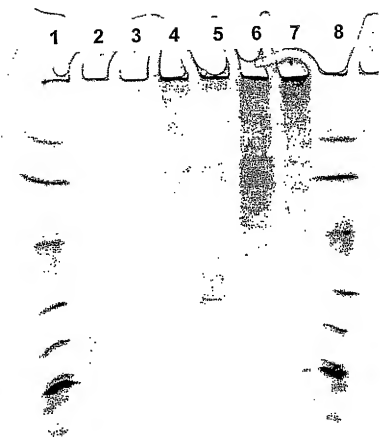


FIG. 164

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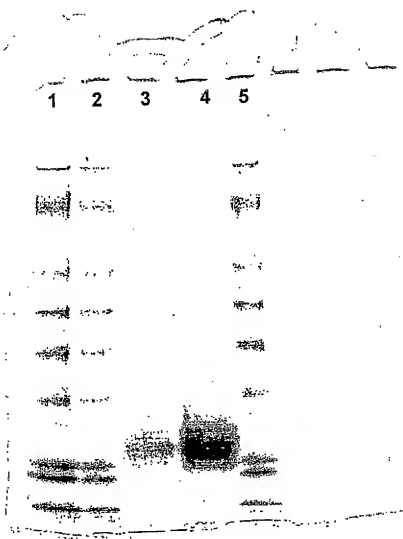


FIG. 165

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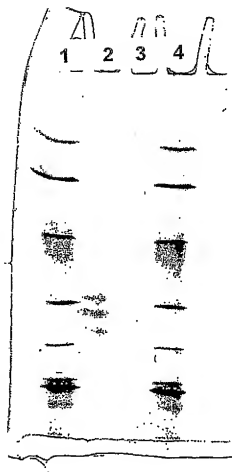


FIG. 166

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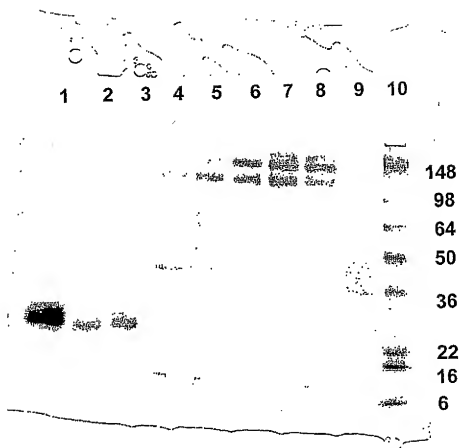


FIG. 167

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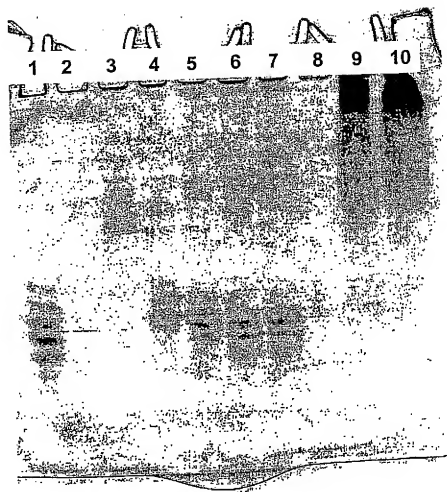


FIG. 168

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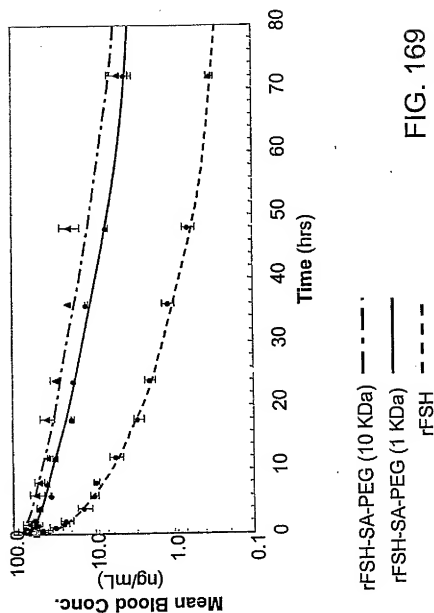


FIG. 169

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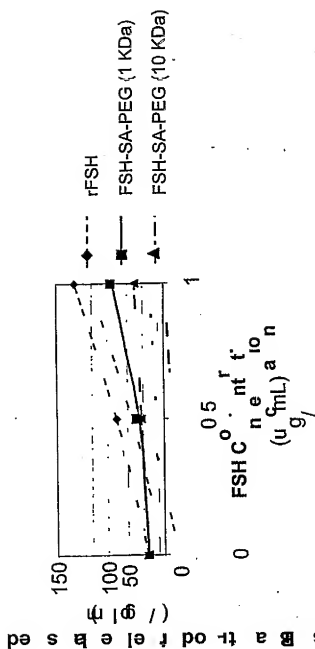


FIG 17

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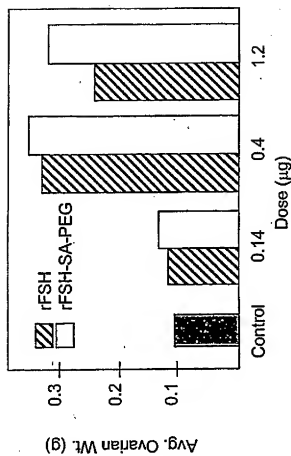


FIG. 171

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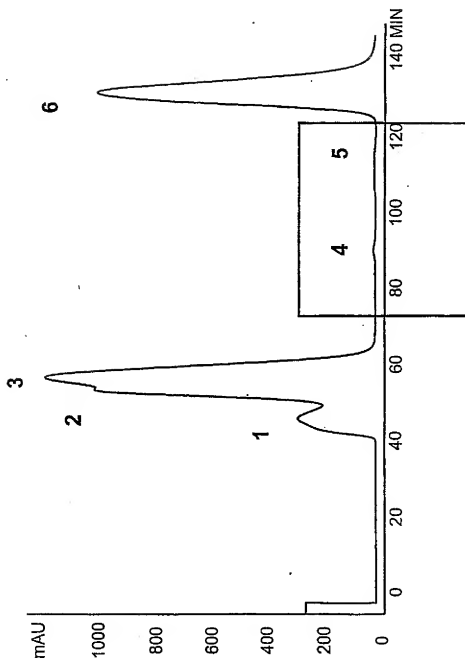


FIG. 172A

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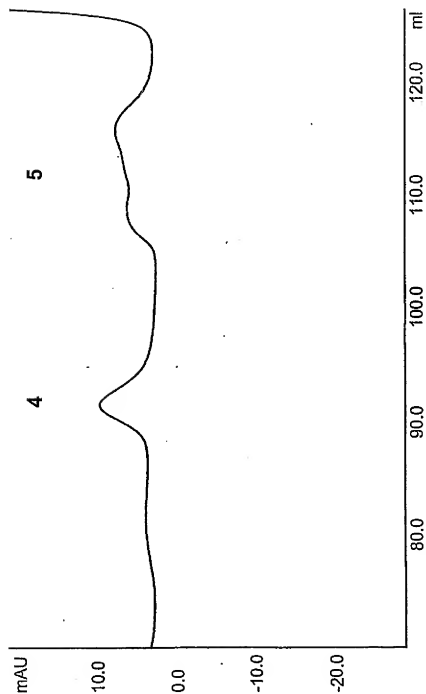


FIG. 172B

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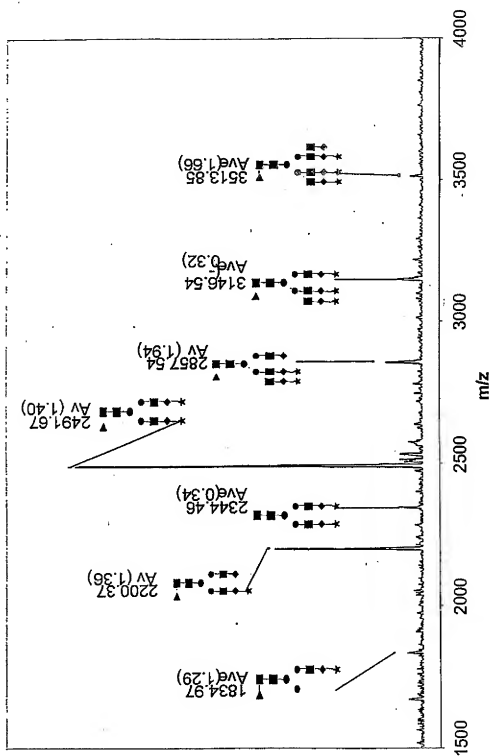


FIG. 173A

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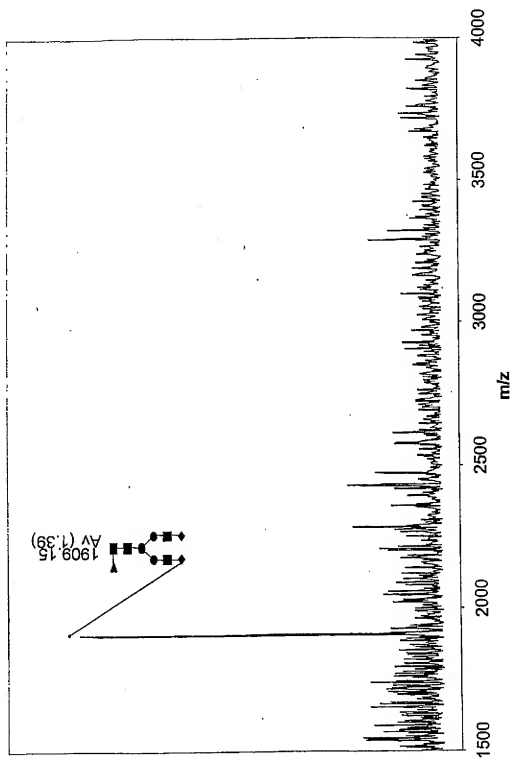


FIG. 173B

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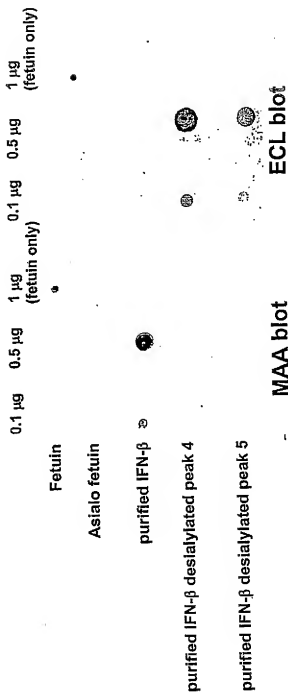


FIG. 174

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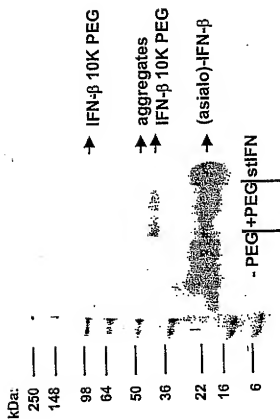


FIG. 175

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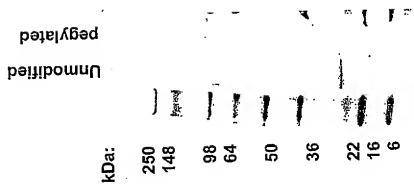


FIG. 176

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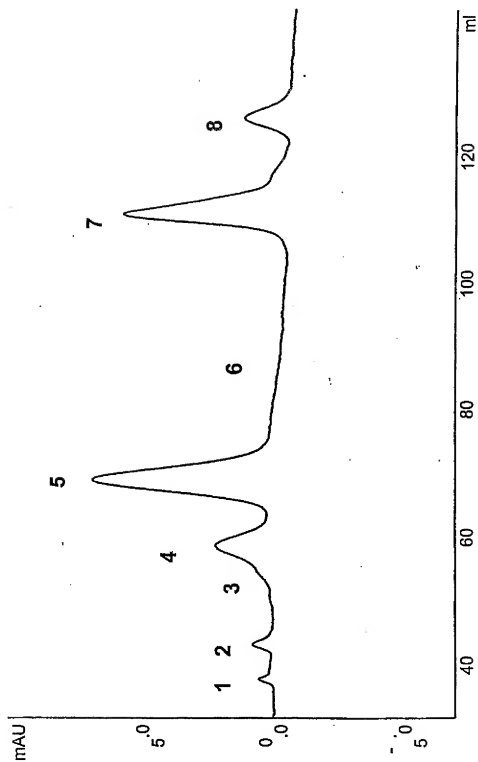
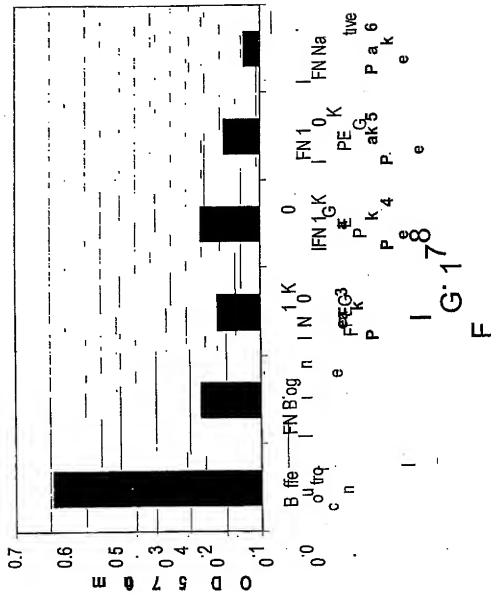
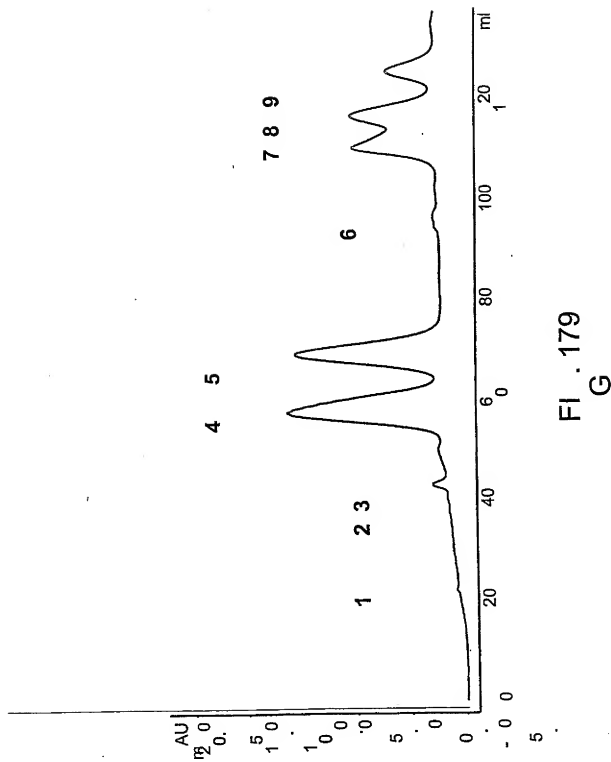


FIG. 177

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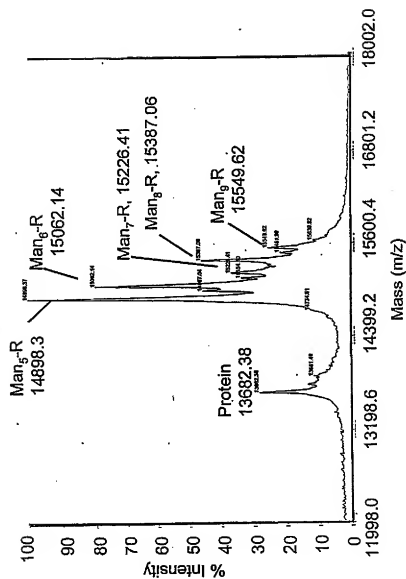


FIG. 180A

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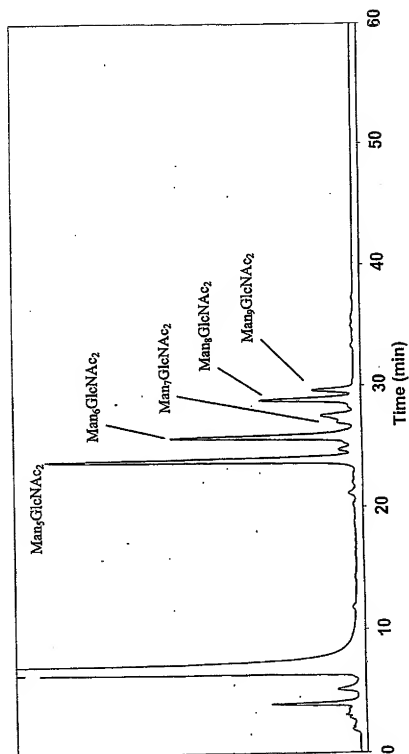
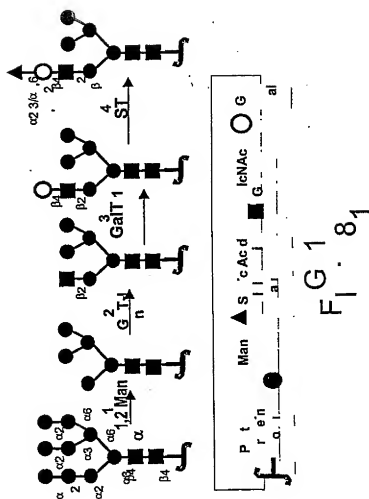


FIG. 180B

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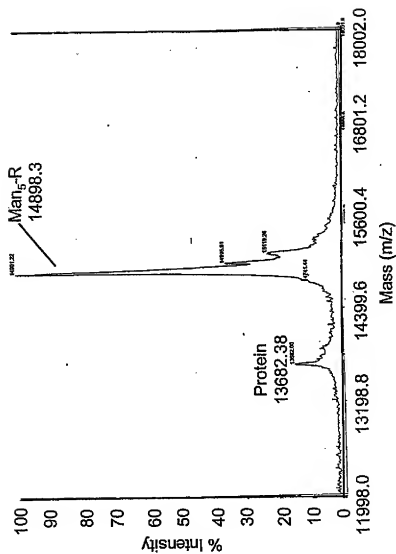


FIG. 182A

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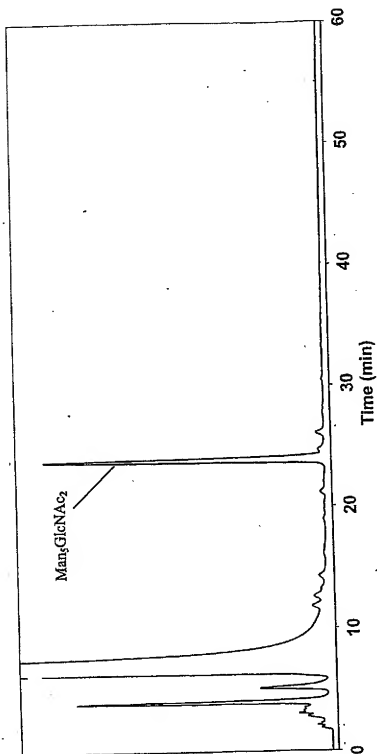
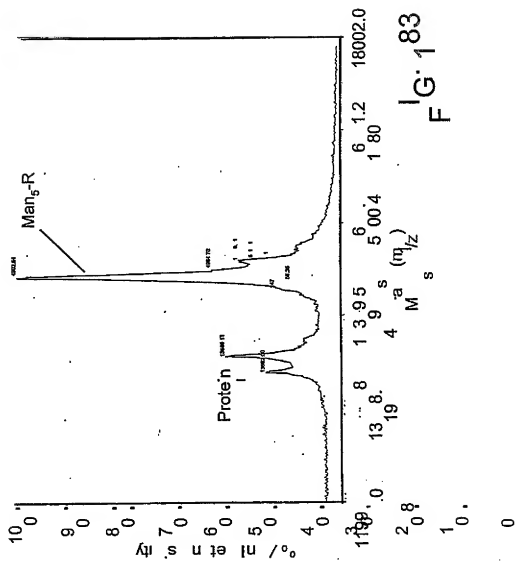


FIG. 182B

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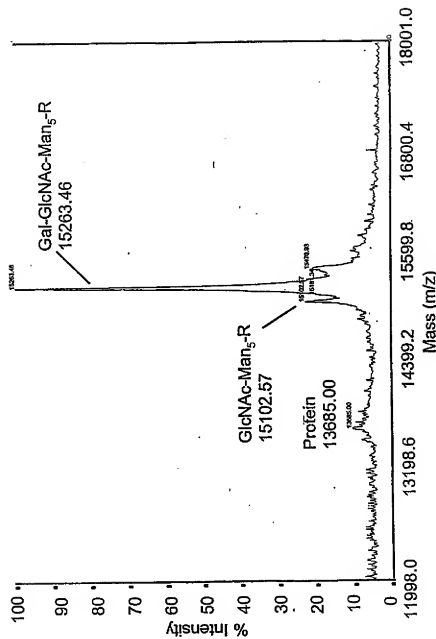
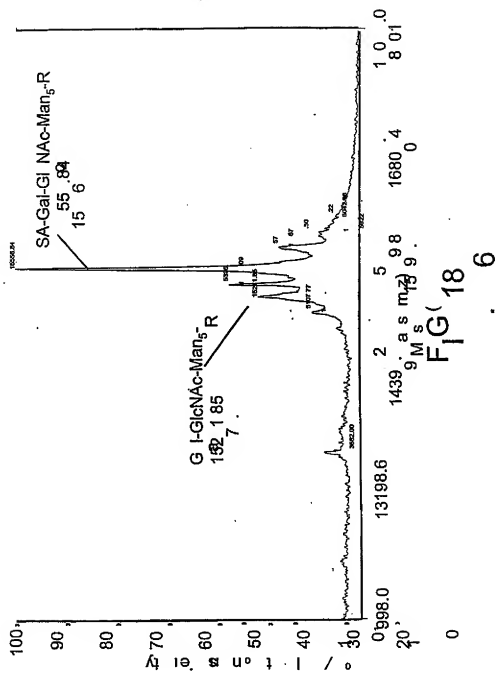


FIG. 185

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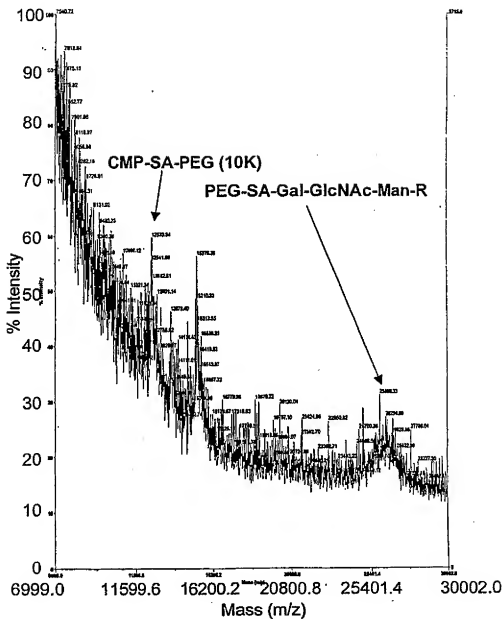
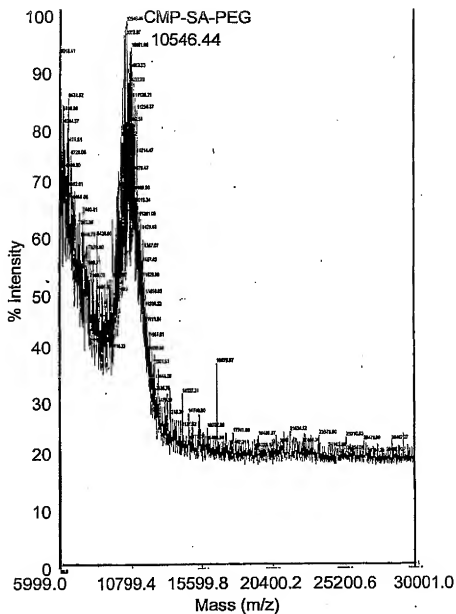


FIG. 187A

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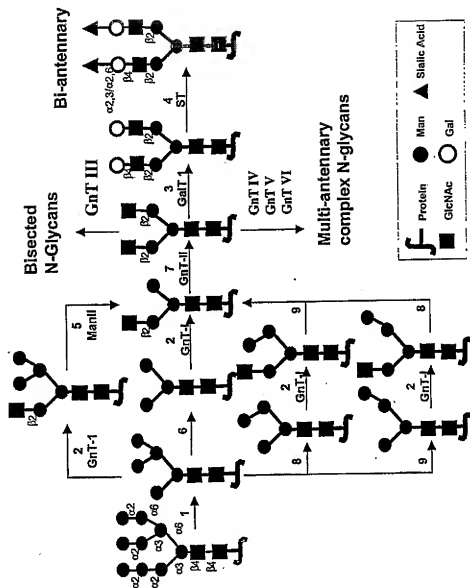
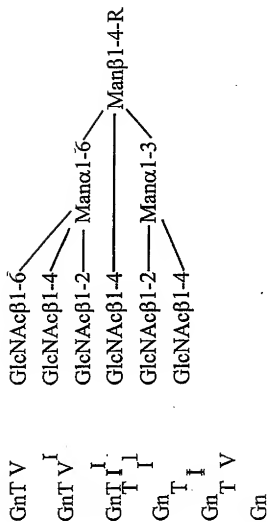


FIG. 188

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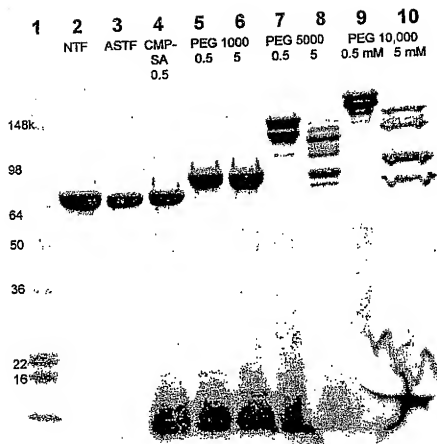


FIG. 190

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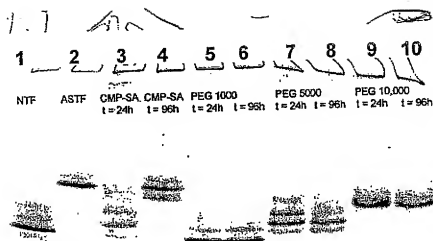


FIG. 191

<110> Neose Technologies, Inc.
DeFrees, Shawn
Zopf, David
Bayer, Robert
Hakes, David
Chen, Xi
Bowe, Caryne

<120> GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE METHODS

<130> 040853-01-5051WO

<150> US 60/328,523
<151> 2001-10-10

<150> US 60/334,233
<151> 2001-11-28

<150> US 60/334,301
<151> 2001-11-28

<150> US 60/344,692
<151> 2001-10-19

<150> US 60/387,292
<151> 2002-06-07

<150> US 60/391,777
<151> 2002-06-25

<150> US 60/396,594
<151> 2002-07-17

<150> US 60/404,249
<151> 2002-08-16

<150> US 60/407,527
<151> 2002-08-28

<150> PCT/US02/32263
<151> 2002-10-09

<150> US 10/360,779
<151> 2003-02-19

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<151> 2003-01-06

<150> US 10/287,994
<151> 2002-11-05

<160> 75

<170> PatentIn version 3.2

<210> 1
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 60

gtgaggaaga tccagggcga tggcgagcgc ctccaggaga agctgtgtgc cacctacaag
 120

ctgtgccacc cagaggagct ggtgctgtc ggacactctc tgggcatccc ctgggctccc
 180

ctgagcaget gcccagcca ggccctgcag ctggcaggct gcttgagcca actccatagc
 240

ggccttttcc tctaccaggg gctcctgcag gccctggaag ggatctcccc cgagttgggt
 300

cccaccttgg acacactgca gctggacgtc gccgactttg ccaccacat ctggcagcag
 360

atggaagaac tgggaatggc cctgcccctg cagccacccc aggggtgcat gccggccttc
 420

gcctctgctt tccagcgccg ggcaggaggg gtctctggtg cctcccatct gcagagcttc
 480

ctggaggtgt cgtaccgcgt tctacgccac ctggccagc cctga
 525

<210> 2
 <211> 174
 <212> PRT
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 Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
 1 5 10 15

Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
 20 25 30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
 35 40 45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
 50 55 60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
 65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
 85 90 95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
 100 105 110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
 115 120 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
 145 150 155 160

Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
 165 170

<210> 3
 <211> 1733
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 <213> Homo sapiens

<400> 3
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 60
 tcaagttaag taaaatgtca atagcctttt aatttaattt ttaattgttt tatcattctt
 120
 tgcaataata aaacattaac ttatatacttt ttaatttaat gtatagaata gagatataca
 180
 taggatatgt aaatagatac acagtgtata tgtgattaaa atataatggg agattcaatc
 240
 agaaaaaagt ttctaaaaag gctctggggg aaaagaggaa' ggaacaata atgaaaaaaa
 300
 tgtgggtgaga aaacacagctg aaaacccatg taaagagtgt ataaagaaag caaaaagaga
 360
 agtagaaaagt aacacagggg catttggaat atgtaaacga gtatgttccc tatttaaggc
 420
 taggcacaaa gcaaggtcct cagagaacct ggagcctaag gtttaggctc acccatttca
 480
 accagtctag cagcatctgc aacatctaca atggccttga cctttgcttt actggtggcc
 540
 ctctgggtgc tcagctgcaa gtcaagctgc tctgtgggct gtgatctgcc tcaaacccac
 600
 agcctgggta gcaggaggac ctgtgatctc ctggcacaga tgaggagaat ctctcttttc
 660
 tctgtcttga aggacagaca tgacttttga ttccccagg aggagtttgg caaccagttc
 720
 caaaaggctg aaaccatccc tgtcctccat gagatgatcc agcagatctt caatctcttc
 780
 agcacaaaag actcatctgc tgcctgggat gagacctcc tagacaaatt ctacactgaa
 840
 ctctaccagc agctgaatga cctggaagcc tgtgtgatac aggggggtggg ggtgacagag
 900
 actcccctga tgaaggagga ctccattctg gctgtgagga aatacttcca aagaatcact
 960

ctctatctga aagagaagaa atacagccct tgtgcctggg aggtgtgcag agcagaaatc
1020

atgagatctt tttctttgtc aacaaacttg caagaaagt tttaagaagtaa ggaatgaaaa
1080

ctggttcaac atggaaatga ttttcattga ttctgtatgcc agctcacctt tttatgatct
1140

gccatttcaa agactcatgt ttctgctatg accatgacac gatttaaato ttttcaaagt
1200

tttttaggag tattaatcaa cattgtattc agctottaag gcactagtcc cttacagagg
1260

accatgctga ctgatccatt atctatttaa atatttttaa aatattattt atttaactat
1320

ttataaaaca aattattttt gttoatatta tgcattgtgc acctttgcac agtggttaat
1380

gtaataaaat gtgttctttg tatttggtta atttattttg tgtgttcoat tgaacttttg
1440

ctatggaact ttgtacttg tttattcttt aaaatgaaat tccaagccta attgtgcaac
1500

ctgattacag aataactggt acaactcatt tgtocatcaa tattatatto aagatataag
1560

taaaaataaa cttttgttaa accaagttgt atgttgtact caagataaca gggatgaacct
1620

aacaaatata attctgtctt cttgtgtatt tgatttttgt atgaaaaaaa ctaaaaatgg
1680

taatcatact taattatcag ttatggtaaa tggatatgaag agaagaagga acg
1733

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<211> 188

<212> PRT

<213> Homo sapiens

<400> 4

Met	Ala	Leu	Thr	Phe	Ala	Leu	Leu	Val	Ala	Leu	Leu	Val	Leu	Ser	Cys
1				5					10					15	

Lys	Ser	Ser	Cys	Ser	Val	Gly	Cys	Asp	Leu	Pro	Gln	Thr	His	Ser	Leu
			20					25					30		

Gly	Ser	Arg	Arg	Thr	Leu	Met	Leu	Leu	Ala	Gln	Met	Arg	Arg	Ile	Ser
		35					40					45			

Leu	Phe	Ser	Cys	Leu	Lys	Asp	Arg	His	Asp	Phe	Gly	Phe	Pro	Gln	Glu
	50					55					60				

Glu	Phe	Gly	Asn	Gln	Phe	Gln	Lys	Ala	Glu	Thr	Ile	Pro	Val	Leu	His
65						70				75					80

Glu Met Ile Gln Glu Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser
85 95

Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr
100 105 110

Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
115 120 125

Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys
130 135 140

Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro
145 150 155 160

Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu
165 170 175

Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu
180 185

<210> 5

<211> 757

<212> DNA

<213> Homo sapiens

<400> 5

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60

tccatgagct acaacttgct tggattccta caaagaagca gcaattttca gtgtcagaag
120

ctctgtggc aattgaatgg gaggttgaa tattgoccca aggacaggat gaactttgac
180

atccctgagg agattaagca gctgcagcag ttccagaagg aggacgccgc attgaccatc
240

tatgagatgc tccagaacat ctttgctatt ttcagacaag attcatctag cactggctgg
300

aatgagacta ttgttgagaa cctcctggct aatgtctatc atcagataaa ccatctgaag
360

acagtctctg aagaaaaact ggagaaagaa gattttacca ggggaaaact catgagcagt
420

ctgcacctga aaagatatta tgggaggatt ctgcattacc tgaaggccaa ggagtacagt
480

cactgtgcct ggaccatagt cagagtggaa atcctaagga acttttactt cattaacaga
540

cttacagggt acctccgaaa ctgaagatct cctagcctgt cctctggga ctggacaatt
600

gcttcaagca ttcttcaacc agcagatgct gtttaagtga ctgatggcta atgtactgca
660

aatgaaaagga caactagaaga ttttgaaatt ttattataat tatgagttat ttttatttat
720

ttaaatttta ttttgaaaa taaattattt ttggtgc
757

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<213> Homo sapiens

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Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
20 25 30
Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
35 40 45
Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
50 55 60
Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
65 70 75 80
Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
85 90 95
Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
100 105 110
Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
115 120 125
Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
130 135 140
Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
145 150 155 160
His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
165 170 175
Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
180 185

<210> 7
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<212> DNA
<213> Homo sapiens

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gcagtctcttg taaccaggga ggaagcccac ggcgctctgc accggcgccg gcgcgccaac
120

gagttccttg aggaagctcgc gccgggctcc ctggagaggg agtgcaagga ggagcagtgcc
180

tccttcgagg agggcccgga gatcttcaag gacgcggaga ggacgaagct gttctgatt
240

tcttacagt atggggacca gtgtgcctca agtccatgcc agaatggggg ctctcgcaag
300

gaccagctcc agtctctatat ctgcttctgc ctccctgctc tcgagggccg gaactgtgag
360

acgcacaagg atgaccagct gatctgtgtg aacgagaacg gccgctgtga gcagtgactgc
420

agtgaaccaca cgggcaccaa gcgctcctgt cggtgccagc aggggtaact tctgctggca
480

gacgggggtg bctgcacacc cacagtgaa tatccatgtg gaaaaatacc tattctagaa
540

aaaagaaatg ccagcaaacc ccaaggccga attgtggggg gcaaggtgtg ccccaaaggg
600

gagtggtccat ggcaggtcct gttgttggtg aatggagctc agttgtgtgg ggggaccctg
660

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720

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780

cggcgggtgg cgcaggtcat catcccagc acgtacgtcc cgggcaccac caaccacgac
840

atcgcgctgc tccgctgca ccagcccggt gtcctcactg accatgtggt gccctctg
900

ctgccgaac ggacgttctc tgagaggagc ctggccttcg tgcgcttctc attggtcagc
960

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ccccggtga tgaccaggga ctgcctgcag cagtcacgga aggtgggaga ctccccaat
1080

atcacggagt acatgttctg tgccggtac tcggatggca gcaaggactc ctgcaagggg
1140

gacagtgag gccacatgc caccactac cggggcacgt ggtacctgac gggcatctg
1200

agctggggcc agggctgcgc aaccgtgggc cactttgggg tgtacaccag ggtctccag
1260

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1320

gccccatttc cc
1332

<210> 8
<211> 444
<212> PRT
<213> Homo sapiens

<400> 8
Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
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Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
20 25 30
Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
35 40 45
Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
50 55 60
Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
65 70 75 80
Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
85 90 95
Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
100 105 110
Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
115 120 125
Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
130 135 140
Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145 150 155 160
Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
165 170 175
Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
180 185 190
Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
195 200 205
Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
210 215 220
Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
225 230 235 240
Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
245 250 255
Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
260 265 270
Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
275 280 285

Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
 290 295 300
 Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
 305 310 315 320
 Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
 325 330 335
 Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
 340 345 350
 Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
 355 360 365
 Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
 370 375 380
 Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
 385 390 395 400
 Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
 405 410 415
 Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
 420 425 430
 Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro
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 <210> 9
 <211> 1437
 <212> DNA
 <213> Homo sapiens
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 120
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 240
 actgaaaaga caactgaatt ttggaagcag tatgttgatg gagatcagtg tgagtccaat
 300
 ccattgtttaa atggcggcag ttgcaaggat gacattaatt cctatgaatg ttgggtgtccc
 360
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 420
 tgcgagcagt tttgtaaaaa tagtgctgat aacaaggtgg ttgtctcctg tactgaggga
 480

tātōgācttg cāgāāaacca gaagtccctgt gaaccagcag tgccatttcc atgtggaaga
540

gtttctgttt cacaaacttc taagctcacc cgtgctgagg ctgtttttcc tgatgtggac
600

tatgtaaatc ctactgaagc tgaaaccaatt ttggataaca tcaactcaagg cacccaatca
660

tttaatgact tcaactcgggt tgttggtgga gaagatgcc aaccagggtca attcccttgg
720

caggttgttt tgaatggtaa agttgatgca ttctgtggag gctctatcgt taatgaaaaa
780

tggattgtaa ctgctgccca ctgtgttgaa actgggtgta aaattacagt tgcgcagggt
840

gaacataata ttgaggagac agaacataca gagcaaaagc gaaatgtgat tcgagcaatt
900

attcctcacc acaactacaa tgcagctatt aataagtaca accatgacat tgcccttctg
960

gaactggagc aacccttagt gctaaacagc tacgttacac ctatttgcat tctgacaag
1020

gaatacacga acatcttctc caaatttga ttggctatg taagtggctg ggcaagagtc
1080

ttccacaaag ggagatcagc tttagtctt cagtacctta gagttccact tgttgaccga
1140

gccacatgtc ttgatctac aaagttcacc atctataaca acatgttctg tgcgtgcttc
1200

catgaaggag gtagagattc atgtcaagga gatagtggg gaccccatgt tactgaagtg
1260

gaagggacca gtttcttaac tggaattatt agctgggggtg aagagtgtgc aatgaaaggc
1320

aaatatggaa tatataccaa ggtatcccg tatgtcaact ggattaagga aaaacaaag
1380

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1437

<210> 10
<211> 462
<212> PRT
<213> Homo sapiens

<400> 10
Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr
1 5 10 15

Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu
25 30

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn

35

40

45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
 50 55 60

Met Glu Glu Lys Cys Ser Phe Glu Glu Pro Arg Glu Val Phe Glu Asn
 65 70 75 80

Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
 85 90 95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
 100 105 110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
 115 120 125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
 130 135 140

Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly
 145 150 155 160

Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe
 165 170 175

Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala
 180 185 190

Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn Pro Thr Glu Ala Glu
 195 200 205

Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser Phe Asn Asp Phe
 210 215 220

Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp
 225 230 235 240

Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile
 245 250 255

Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly
 260 265 270

Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu
 275 280 285

His Thr Glu Gln Lys Arg Asn Val Ile Arg Ala Ile Ile Pro His His
 290 295 300

Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu
 305 310 315 320

Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys
 325 330 335

Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly
 340 345 350

Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu
 355 360 365

Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu
 370 375 380

Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe
 385 390 395 400

His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His
 405 410 415

Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp
 420 425 430

Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val
 435 440 445

Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr
 450 455 460

<210> 11

<211> 603

<212> DNA

<213> Homo sapiens

<400> 11

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gtttccatt ccgctcctga tgtgcaggat tgcccagaat gcacgctaca ggaaaacca
 120

ttcttctccc agccgggtgc cccaatactt cagtgcattg gctgctgctt ctctagagca
 180

tatccactc cactaaggtc caagaagacg atgttggtcc aaaagaacgt cacctcagag
 240

tccacttgct gtgtagctaa atcatataac agggtcacag taatgggggg tttcaaagt
 300

gagaaccaca cggcgtgcc aatgcagtact tgttattatc acaaatotta aatgttttac
 360

caagtgcgtg cttgatgact gctgatttct tggaatggaa aattaagttg tttagtgttt
 420

atggctttgt gagataaaac totccttttc cttaccatac cacttttgaca cgcttcaagg
 480

atatactgca gctttactgc cttcctcgtt atcctacagt acaatcagca gtctagttct
 540

tttctatttg aatgaataca gcattaagct tgttccactg caaataaagc cttttaaatc
 600

atc

603

<210> 12

<211> 116

<212> PRT

<213> Homo sapiens

<400> 12

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
1 5 10 15Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
20 25 30Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
35 40 45Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
50 55 60Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
65 70 75 80Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
85 90 95Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
100 105 110Tyr His Lys Ser
115

<210> 13

<211> 390

<212> DNA

<213> Homo sapiens

<400> 13

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60tgtgagctga ccaacatcac cattgcaata gagaagaag aatgtcgttt ctgcataagc
120atcaacacca ctgtgtgtgc tggctactgc tacaccaggg atctggtgta taaggaccca
180gccaggccca aaatccagaa aacatgtacc ttcaaggaac tggtatatga aacagtgaga
240gtgcccggt gtgctcacca tgcagattcc ttgtatacat acccagtggc caccagtggt
300cactgtggca agtgtgacag cgacagcact gattgtactg tgcgaggcct ggggccacgc
360tactgtcct ttggtgaaat gaaagaataa
390

<210> 14

<211> 129

<212> PRT

<213> Homo sapiens

<400> 14

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile

1 5 10 15

Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys
20 25 30

Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly
35 40 45

Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys
50 55 60

Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg
65 70 75 80

Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val
85 90 95

Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
100 105 110

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys
115 120 125

Glu

<210> 15
<211> 1342
<212> DNA
<213> Homo sapiens

<400> 15
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cgcacctctc ctccaggccc gtgggggttg cctgcacgg ccgagcttcc cgggatgagg
120

gccccgggtg tggtaaccgg gcgcgcccca ggtogctgag ggaccccgcc caggcgcgga
180

gatgggggtg cacgaatgtc ctgcctggct gtggcttctc ctgtccctgc tgtogctccc
240

tctgggcctc ccagtctggg gcgccccacc aagcctcctc tgtgacagcc gactcctgga
300

gagggtacctc ttggaggcca aggaggccga gaatatcagc acgggctgtg ctgaacctg
360

cagcttgaat gagaatatca ctgtcccaga caccaaagtt aatttctatg cctggaagag
420

gatggaggtc gggcagcagg ccgtagaagt ctggcagggc ctggccctgc tgtcggaagc
480

tgctctgcgg ggccaggccc tgttggtcaa ctcttccag ccgtgggagc cctgcagct
540

gcattgtgat aaagcgtca gtggccttgc cagcctcacc actctgcttc gggctctgcg
600

agcccagaag gaagccatct ccctccaga tgcggcctca gctgctccac tccgaacaat
 660
 cactgtctgac acttttcogca aactcttccg agtctactcc aatttctctcc ggggaaagct
 720
 gaagctgtac acagggggagg cctgcaggac aggggacaga tgaccagggt tgtccacctg
 780
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 900
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 960
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 1080
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 1140
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 1200
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 1260
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 1320
 aaaccaccaa aaaaaaaaaa aa
 1342

<210> 16
 <211> 193
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu
 1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
 20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
 35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
 50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu
130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
180 185 190

Arg

<210> 17
<211> 435
<212> DNA
<213> Homo sapiens

<400> 17
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cgctcgccca gccccagcac gcagccctgg gagcatgtga atgccatcca ggaggcccg
120
cgtctcctga acctgagtag agacactgct gctgagatga atgaaacagt agaagtcac
180
tcagaaatgt ttgacctoca ggagccgacc tgcctacaga cccgcctgga gctgtacaag
240
cagggcctgc ggggcagcct caccagctc aagggcccct tgaccatgat ggccagccac
300
tacaagcagc actgccctcc aaccccgaa acttctctgt caaaccagat tatcaccttt
360
gaaagtttca aagagaaact gaaggacttt ctgcttgta tccccttga ctgctgggag
420
ccagtcagg agtga
435

<210> 18
<211> 144
<212> PRT
<213> Homo sapiens

<400> 18
Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile

1 5 10 15

Ser Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His
20 25 30

Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp
35 40 45

Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe
50 55 60

Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys
65 70 75 80

Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met
85 90 95

Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
100 105 110

Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys
115 120 125

Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
130 135 140

<210> 19
<211> 501
<212> DNA
<213> Homo sapiens

<400> 19
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tgttactgcc aggaccata tgtaaaagaa gcagaaaacc ttaagaaata ttttaatgca
120

ggtcattcag atgtagcgga taatggaact cttttotttag gcattttgaa gaattggaaa
180

gaggagagtg acagaaaaat aatgcagagc caaattgtct cttttactt caaacttttt
240

aaaaacttta aagatgacca gagcatocaa aagagtgtgg agaccatcaa ggaagacatg
300

aatgtcaagt ttttcaatag caacaaaaag aaacgagatg acttcgaaaa gctgactaat
360

tattcggtaa ctgacttgaa tgtccaacgc aaagcaatac atgaactcat ccaagtgatg
420

gctgaactgt cgccagcagc taaaacaggg aagcgaaaaa ggagtcagat gctgtttcga
480

ggtcgaagag catcccagta a
501

<210> 20
<211> 166

<212> PRT
 <213> Homo sapiens

<400> 20

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
 1 5 10 15

Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu
 20 25 30

Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
 35 40 45

Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
 50 55 60

Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
 65 70 75 80

Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile
 85 90 95

Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
 100 105 110

Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val
 115 120 125

Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
 130 135 140

Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg
 145 150 155 160

Gly Arg Arg Ala Ser Gln
 165

<210> 21

<211> 1352

<212> DNA

<213> Homo sapiens

<400> 21

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cctgtgtctgc ctggtccctg tctccctggc tgaggatccc caggagatg ctgccacaga
 120

gacagatata tcccaccatg atcaggatca cccaaccttc aacaagatca cccccaacct
 180

ggctgagttc gccttcagcc tataccgcc gctggcacac cagtcaca gcaccaatat
 240

cttctctctcc ccagttagca tcgctacagc ctttgcaatg ctctccctgg ggaccaaggc
 300

tgacactcac gatgaaatcc tggaggccct gaatttcaac ctacaggaga ttccggaggc
 360

tcagatccat gaaggcttcc aggaactcct cagtaccctc aaccagccag acagccagct
420

ccagctgacc accggcaatg gcctgttccct cagcgagggc ctgaagctag tggataagtt
480

tttggaggat gttaaaaagt tgtaccactc agaagccttc actgtcaact toggggacac
540

cgaagaggcc aagaacaga tcaacgatta cgtggagaag ggtactcaag ggaaaattgt
600

ggatttggtc aaggagcttg acagagacac agtttttgtc ctggtgaatt acatcttctt
660

taaaggcaaa tgggagagac cctttgaagt caaggacacc gaggaagagg acttccacgt
720

ggaccagtg accacogtga aggtgcctat gatgaagcgt ttaggcattgt ttaacatcca
780

gcactgtaag aagctgtcca gctgggtgct gctgatgaaa tacctgggca atgccaccgc
840

catcttcttc ctgcctgatg aggggaaact acagcactcg gaaaatgaac tcaccacaga
900

tatcatcacc aagtctctgg aaaatgaaga cagaaggctc gccagcttac atttaccocaa
960

actgtccatt actggaacct atgatctgaa gagcgtcctg ggtcaactgg gcatcaactaa
1020

ggtcttcagc aatggggctg acctctccgg ggtcacagag gaggcacccc tgaagctctc
1080

caaggccgtg cataaggctg tgctgacct cgcagagaaa gggactgaag ctgctggggc
1140

catgttttta gagccatac ccatgtctat cccccccgag gtcaagttca acaaacctt
1200

tgtcttctta atgattgaac aaaataccaa gtctccctc ttcattggaa aagtgtgaa
1260

tcccacccaa aaataactgc ctctcgtctc tcaacccctc cctccatcc ctggccccct
1320

cctgggatga cattaagaa gggttgagct gg
1352

<210> 22
<211> 418
<212> PRT
<213> Homo sapiens

<400> 22
Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys
1 5 10 15
Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala

20

25

30

Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
35 40 45

Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
50 55 60

Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
65 70 75 80

Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
85 90 95

His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro
100 105 110

Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
115 120 125

Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
130 135 140

Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
145 150 155 160

Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
165 170 175

Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
180 185 190

Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
195 200 205

Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
210 215 220

Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val
225 230 235 240

Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
245 250 255

Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
260 265 270

Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
275 280 285

Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
290 295 300

Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
305 310 315 320

Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
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Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
340 345 350

Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
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 Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
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 <213> Homo sapiens

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<212> PRT
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Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu
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Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
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Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
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Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
115 120 125
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Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
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Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
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Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
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Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
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Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
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Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro
225 230 235 240
Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu
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Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu
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Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu

275

280

285

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 Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu
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 Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr
 325 330 335
 Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr
 340 345 350
 Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
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 370 375 380
 Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
 385 390 395 400
 Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
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 Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
 420 425 430
 Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp
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 Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
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 Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys
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 Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
 485 490 495
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<211> 1726

<212> DNA

<213> Homo sapiens

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<211> 562

<212> PRT

<213> Homo sapiens

<400> 26

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Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
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Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
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Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr
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Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu
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Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr
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Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser
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Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro
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Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His
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Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val

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Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val
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 Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys Gln Leu Gln
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 Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
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Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
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Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
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His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
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Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
130 135 140
Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
145 150 155 160
Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
165 170 175
Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
180 185 190
Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr

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Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly 210 215 220		
Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp 225 230 235 240		
Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr 245 250 255		
Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val 260 265 270		
Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile 275 280 285		
Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser 290 295 300		
Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met 305 310 315 320		
Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His 325 330 335		
Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro 340 345 350		
Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp 355 360 365		
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Trp Val His Tyr Ile Ala Ala Glu Glu Asp Trp Asp Tyr Ala Pro 405 410 415		
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Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met 435 440 445		
Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu 450 455 460		
Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu 465 470 475 480		
Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro 485 490 495		
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Pro Phe	Leu Arg	Val Ala	Thr	Glu Ser	Ser Ala	Lys	Thr Pro	Ser	1565	1570	1575
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Pro Gly	Val Phe Glu Thr Val	Glu Met Leu Pro Ser	Lys Ala Gly
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Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys 2255 2260 2265		
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Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val 2300 2305 2310		
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cggctcagag aatactatga ccagacagct cagatgtgct gcagcaaatg ctgcggggc
180
caacatgcaa aagtcttctg taccaagacc tcggacaccg tgtgtgactc ctgtgaggac
240
agcacatata ccagctctg gaactgggtt ccgagtgct tgagctgtgg ctcccgctgt
300
agctctgacc aggtggaac tcaagcctgc actcgggaac agaaccgat ctgcacctgc
360
aggcccggt ggtactgccc gctgagcaag caggaggggt gccggtgtg cgcccgctg
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600
acgtccacgt cccccaccg gagtatggcc ccagggcgag tacacttacc ccagccagtg
660
tccacacgat cccaacacac gcagccaact ccagaaccga gcactgctcc aagcacctcc
720
ttcctgctcc caatgggcc cagccccca gctgaaggga gcactggcga ctctcgtctt
780
ccagttggac tgatttgagg tgtgacagcc ttgggtctac taataatagg agtgggtaac
840
tgtgtcatca tgaccagggt gaaaaagaag cccttgctgc tcgagagaga agccaagggtg
900
cctcacttgc ctgcgataa ggcccggggt acacagggcc ccgagcagca gcacctgctg
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atcacagcgc cgagctccag cagcagctcc ctggagagct cggccagtgc gttggacaga
1020
agggcgccca ctcggaacca gccacaggca ccaggcgtgg aggcagtgg ggcgggggag
1080
gccggggcca gcaccgggag ctgagattct tccctggtg gccatgggac ccaggtcaat
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1200

gccagctcca caatgggaga cacagattcc agccctcgg agtccccgaa ggacgagcay
1260

gtcccttct ccaaggagga atgtgcttt cggtcacagc tggagacgcc agagacccg
1320

ctggggagca ccgaagagaa gccctgccc ottggagtgc ctgatgctgg gatgaagccc
1380

agttaaccag gccggtgtgg gctgtgtogt agccaaggtg ggctgagccc tggcaggatg
1440

accctgcgaa ggggccctgg tccctccagg c
1471

<210> 32
<211> 461
<212> PRT
<213> Homo sapiens

<400> 32
Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
1 5 10 15
Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
20 25 30
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
35 40 45
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50 55 60
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65 70 75 80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
85 90 95
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
100 105 110
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
115 120 125
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
130 135 140
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145 150 155 160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
165 170 175
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
180 185 190
Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
195 200 205
Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser

210 215 220

Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser :
225 230 235 240

Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
245 250 255

Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
260 265 270

Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
275 280 285

Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
290 295 300

Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
305 310 315 320

Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
325 330 335

Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
340 345 350

Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
355 360 365

Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
370 375 380

Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
385 390 395 400

Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
405 410 415

Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
420 425 430

Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
435 440 445

Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
450 455 460

<210> 33
<211> 1475
<212> DNA
<213> Homo sapiens

<400> 33
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agcgccccga cctcgccacc atgagagccc tgctggcgcg cctgcttctc tgcgtcctgg
120
tcgtgagcga ctccaaagcg agcaatgaac ttcataaagt tccatogaac tgtgactgtc
180

taaatggagg aacatgtgtg tocaacaagt acttctccaa cattcactgg tgcaactgcc
240

caaagaaatt cggaggggcag cactgtgaaa tagataagtc aaaaacctgc tatgagggga
300

atggtcactt ttaccgagga aaggccagca ctgacaccaa gggcggggcc tgccctgocct
360

ggaactctgc cactgtcctt cagcaaacgt accatgcccc cagatctgat gctcttcagg
420

tgggcctggg gaaacataat tactgcagga acccagacaa cgggaggcga cccctggtgct
480

atgtgcaggt gggcctaaag ccgcttgtcc aagagtgcac ggtgcatgac tgccgagatg
540

gaaaaaagcc ctccctctct ccagaagaat taaaatttca gtgtggccaa aagactctga
600

ggcccccgtt taagattatt gggggagaat tcaccaccaa cgagaaccag cccctggttg
660

cggccatcta caggaggcac cgggggggct ctgtcaccta cgtgtgtgga ggcagcctca
720

tcagcccttg ctgggtgatc agcgcacac actgcttcat tgattaccca aagaaggagg
780

actacatcgt ctacctgggt cgtcgaagg ttaactccaa cagcgaagg gagatgaagt
840

ttgaggtgga aaacctcctc ctacacaagg actacacgc tgacacgctt gctcaccaca
900

acgacattgc cttgtctgaag atccgttcca aggaggcag gtgtgcgcag ccatccggga
960

ctatacagac catctgcctg ccctcgatgt ataacgatcc ccagtttggc acaagctgtg
1020

agatcactgg ctttgaaaaa gagaattcta ccgactatct ctatccggag cagctgaaga
1080

tgactgttgt gaagctgatt tcccacggg agtgtcagca gccccactac tacggctctg
1140

aagtcaccac caaaatgctg tgtgtgtgctg acccacagt gaaaacagat tcctgccaag
1200

gagactcagg gggacccctc gtctgttccc tccaaggcag catgactttg actggaattg
1260

tgagctgggg ccgtggatgt gccctgaagg acaagccagg cgtctacacg agagtctcac
1320

acttcttacc ctggatccgc agtcacacca aggaagagaa tggcctggcc ctctgagggg
1380

ccccagggag gaaacgggca ccaccogctt tcttgctggt tgcattttt gcagtagagt
1440

catctccatc agctgtaaga agagactggg aagat
1475

<210> 34
<211> 431
<212> PRT
<213> Homo sapiens

<400> 34
Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
1 5 10 15
Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
20 25 30
Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
35 40 45
His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
50 55 60
Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
65 70 75 80
Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
85 90 95
Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
100 105 110
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
115 120 125
Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
130 135 140
Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
145 150 155 160
Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
165 170 175
Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp
180 185 190
Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val
195 200 205
Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His
210 215 220
Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly
225 230 235 240
Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val
245 250 255
Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His

260

265

270

His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys
 275 280 285
 Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr
 290 295 300
 Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
 305 310 315 320
 Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val
 325 330 335
 Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly
 340 345 350
 Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys
 355 360 365
 Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu
 370 375 380
 Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys
 385 390 395 400
 Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu
 405 410 415
 Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
 420 425 430

 <210> 35
 <211> 107
 <212> PRT
 <213> Mus musculus

 <400> 35
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
 20 25 30
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 36
 <211> 120

<212> PRT

<213> Mus musculus

<400> 36

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
 20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 37

<211> 120

<212> PRT

<213> Mus musculus

<400> 37

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30

Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80

Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 38

<211> 106

<212> PRT

<213> Mus musculus

<400> 38

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 39

<211> 1039

<212> DNA

<213> Homo sapiens

<400> 39

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ttttctttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag
 120

cattctcgtc atctctgagg*acatcaccat catctcagga tgaggggcat gaagctgctg
 180

ggggcgctgc tggcactggc ggccctactg cagggggcgc tgtccctgaa gatcgacagc
 240

ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt
 300

gtgcagatcc tgagccgcta tgacatgcc ctggctcagg aggtcagaga cagccacctg
 360

actgcogtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac
 420

gtggtcagtg agccactggg acggaacagc tataaggagc gctacotgtt cgtgtacagg
 480

cctgaccagg tgtctcgogt ggacagctac tactacgatg atggctgcga gccctgoggg
 540

aaagacacct tcaaccgaga gccagccatt gtcagggttct tctccgggtt cacagaggtc
 600

agggagtttg cattgtttcc cctgcatgog gccccggggg acgcagtagc cgagatcgac
660

gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttgaggga cgtcatgttg
720

atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtgggc atccatccgc
780

ctgtggacaa gccccacatt ccagtggctg atccccgaca gcgctgacac cacagctaca
840

cccacgcact gtgcctatga caggatcgtg gttgcaggga tgctgctccg aggcgcggtt
900

gttcccgact cggctctttcc ctttaacttc caggctgcct atggcctgag tgaccaactg
960

gcccagcca tcaatgacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc
1020

cacaccagtt gaactgcag
1039

<210> 40

<211> 282

<212> PRT

<213> Homo sapiens

<400> 40

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu
1 5 10 15

Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr
20 25 30

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
35 40 45

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp
50 55 60

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
65 70 75 80

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
85 90 95

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
100 105 110

Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
115 120 125

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe
130 135 140

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
145 150 155 160

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val

165

170

175

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn
180 185 190

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu
195 200 205

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr
210 215 220

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
225 230 235 240

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn
245 250 255

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser
260 265 270

Asp His Tyr Pro Val Glu Val Met Leu Lys
275 280

<210> 41
<211> 678
<212> DNA
<213> Mus musculus

<400> 41
gacatcttgc tgactcagtc tccagccatc ctgtctgtga gtccaggaga aagagtcagt
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ttctcctgca gggccagtc gttcgttggc tcaagcatcc actggtatca gcaagaaca
120
aatggttctc caaggcttct cataaagtat gcttctgagt ctatgtcttg gatcccttc
180
aggttttagtg gcagtggatc agggacagat tttactctta gcatcaacac tgtggagtct
240
gaagatattg cagattatta ctgtcaacaa agtcatagct ggccattcac gttcggctcg
300
gggacaaatt tggaagtaaa agaagtgaag cttgaggagt ctggaggagg cttggtgcaa
360
cctggaggat coatgaaact ctctgtgtt gcctctggat tcattttcag taaccactgg
420
atgaactggg tccgccagtc tccagagaag gggcttgagt gggttgctga aattagatca
480
aaatctatta attctgcaac acattatgag gactctgtga aaggaggtt caccatctca
540
agagatgatt ccaaaagtc tgtctacctg caaatgaccg acttaagaac tgaagacact
600
ggcgtttatt actgttccag gaattactac ggtagtacct acgactactg gggccaaggc
660

accactctca cagtctcc
678

<210> 42
<211> 226
<212> PRT
<213> Mus musculus

<400> 42
Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
1 5 10 15
Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
20 25 30
Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45
Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
65 70 75 80
Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
85 90 95
Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu
100 105 110
Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser
115 120 125
Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His Trp Met Asn Trp Val
130 135 140
Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Ser
145 150 155 160
Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu Ser Val Lys Gly Arg
165 170 175
Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr Leu Gln Met
180 185 190
Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg Asn
195 200 205
Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
210 215 220
Val Ser
225
<210> 43
<211> 450
<212> DNA
<213> Homo sapiens
<400> 43

gtgcatcag aagagcccat caagcacatc actgtccttc tgccatggcc ctgtggatgc
60

gcctcctgcc cctgtctggcg ctgctggccc tctggggacc tgaccagcc gcagcctttg
120

tgaaccaaca cctgtgcggc tcacacctgg tggaagctct ctacctagtg tgcggggaac
180

gaggcttctt ctacacacc aagaccogcc gggaggcaga ggacctgcag gtggggcagg
240

tggagctggg cgggggccct ggtgcaggca gcctgcagcc cttggcctg gaggggtccc
300

tgcagaagcg tggcattgtg gaacaatgct gtaccagcat ctgctccctc taccagctgg
360

agaactactg caactagacg cagcccgag gcagccccc acccgccgcc tctgcaccg
420

agagagatgg aataaagccc ttgaaccagc
450

<210> 44
<211> 110
<212> PRT
<213> Homo sapiens

<400> 44
Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
1 5 10 15
Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly
20 25 30
Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
35 40 45
Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
50 55 60
Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
65 70 75 80
Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
85 90 95
Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
100 105 110

<210> 45
<211> 1203
<212> DNA
<213> Hepatitis B virus

<400> 45
atgggaggtt ggtcttccaa acctcgacaa ggcattggga cgaatcttct tgttcccaat
60

cctctgggat tctttccoga tcaccagttg gacctgogt toggagccaa ctccacaaat
120

ccagattggg acttcaacco caacaaggat cactggccag aggcaatcaa ggtaggagcg
180

ggagacttog ggccagggtt caccacca caoggggtc tttgggggtg gagccctcag
240

gctcagggca tattgacaac agtgccagca gcgctctctc ctgtttccac caatcggcag
300

tcaggaagac agcctactcc catctctcca cctctaagag acagtcattc tcaggccatg
360

cagtggaaact ccacaacatt ccaccaagct ctgctagatc ccagagttag gggcctatat
420

tttctgctg gtggctccag ttccggaaca gtaaacctg ttccgactac tgtctaccc
480

atatogcaa tcttctcgag gactggggac cctgcaccga acatggagag cacaacatca
540

ggattcctag gacctctgt cgtgttacag ggggggttt tottggtgac aagaatcctc
600

acaataccac agagtctaga ctctgtgttg acttctctca attttctagg gggagcacc
660

acgtgtctg gccaaaattc gcagtcacca acctccaac actcacaac ctctgtctc
720

ccaatttgc ctggttatog ctggatgtgt ctgcggggtt ttatcatatt cctcttcac
780

ctgtctgtat gctcatctt ctgtttggtt cttctggact accaaggat gttgccggt
840

tgctctctac ttccaggaac atcaactacc agcacgggac catgcaagac ctgcacgatt
900

cctgtcaag gaacctctat gtttctctt tgttgctgta caaaacctc ggacggaaac
960

tgcacttgta ttccatccc atcatctctg gctttogcaa gattcctatg ggagtgggc
1020

tcagtcggtt tctcctggt cagtttacta gtgcatttg ttcagtgtt cgcagggtt
1080

tcctccactg tttggtttc agttatatg atgatgtgtt attgggggcc aagtctgtac
1140

aacatottga gtccotttt acctctatta ccaattttc tttgtcttg ggtatacat
1200

tga
1203

<210> 46

<211> 400
 <212> PRT
 <213> Hepatitis B virus

<400> 46

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
 35 40 45

Lys Asp His Trp Pro Glu Ala Ile Lys Val Gly Ala Gly Asp Phe Gly
 50 55 60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
 65 70 75 80

Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Val Ser
 85 90 95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu
 100 105 110

Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
 115 120 125

Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
 130 135 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro
 145 150 155 160

Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu
 165 170 175

Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
 180 185 190

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
 195 200 205

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
 210 215 220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
 225 230 235 240

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
 245 250 255

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
 260 265 270

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
 275 280 285

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly
 290 295 300

Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
305 310 315 320

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
325 330 335

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
340 345 350

Phe Val Gln Trp Phe Ala Gly Leu Ser Pro Thr Val Trp Leu Ser Val
355 360 365

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
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Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
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<210> 47

<211> 799

<212> DNA

<213> Homo sapiens

<400> 47

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120

cccaaccatt cccttatcca ggcttttga caacgctatg ctcogcgccc atcgtctgca
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ccagctggcc ttgacacct accaggagtt tgaagaagcc tatatccaa aggaacagaa
240

gtattcattc ctgcagaacc ccagacctc cctctgttcc tcagagtcta ttcgacacc
300

ctccaacagg gaggaacac aacagaaac caacctagag ctgctccgca tctccctgct
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420

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540

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600

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<210> 48
<211> 217
<212> PRT
<213> Homo sapiens

<400> 48
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Ser Arg Pro Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln
35 40 45
Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys
50 55 60
Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe
65 70 75 80
Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys
85 90 95
Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
100 105 110
Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val
115 120 125
Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu
130 135 140
Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg
145 150 155 160
Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser
165 170 175
His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe
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Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys
195 200 205
Arg Ser Val Glu Gly Ser Cys Gly Phe
210 215

<210> 49
<211> 963
<212> DNA
<213> Homo sapiens

<400> 49

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420

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540

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600

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660

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tga
963

<210> 50
<211> 320
<212> PRT
<213> Homo sapiens

<400> 50
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Gly Ser Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg

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 35 40 45
 Leu Val Arg His Cys Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro
 50 55 60
 Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro
 65 70 75 80
 Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val Asp Lys Thr
 85 90 95
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 100 105 110
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 115 120 125
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 130 135 140
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 145 150 155 160
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 165 170 175
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 180 185 190
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 195 200 205
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 210 215 220
 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 225 230 235 240
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 245 250 255
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 260 265 270
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 275 280 285
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
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 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 305 310 315 320

<210> 51
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 51
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 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
 100 105

<210> 52
 <211> 107
 <212> PRT
 <213> Mus musculus

<400> 52
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 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Ile Val Lys Leu Leu Ile
 35 40 45
 Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
 65 70 75 80
 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 53
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 53
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
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 20 25 30

Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 54

<211> 119

<212> PRT

<213> Mus musculus

<400> 54

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr
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20 25 30

Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ala
115

<210> 55

<211> 214

<212> PRT

<213> Homo sapiens

<400> 55

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Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

64

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125
 Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140
 Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160
 Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175
 Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190
 Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 195 200 205
 Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220
 Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 225 230 235 240
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 245 250 255
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 325 330 335
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 340 345 350
 Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 385 390 395 400
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Ser Pro Gly
 435 440 445

<210> 57
 <211> 8540
 <212> DNA
 <213> Homo sapiens

<400> 57
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1380

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<210> 63
<211> 1395
<212> DNA
<213> Homo sapiens

<400> 63
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120
acagccaagc gcggggacat tcccatgaat cccatgtgca ttaccgctc ccgggagaag
180
aaggcaactg aggatgaggg ctgagaacag aagatcccg aggccaccaa cggcggtgtc
240
tgggaactgt ccaaggccaa ttcccgcttt gctaccactt totatcagca cctggcagat
300
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360
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420
gacaccatat ctgagaaaac atctgatcag atccacttct tctttgcaa actgaactgc
480
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540
gacaaatccc ttacottcaa tgagacctac caggacatca gtgagttggt atatggagcc
600
aagotccagc ccotggactt caaggaaaat gcagagcaat ccagagcggc catcaacaaa
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720
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780
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960
gagaagagcc tggccaaggt ggagaaggaa ctcaccccag aggtgtctga ggagtggctg
1020
gatgaattgg aggagatgat gctggtggtc cacatgcccc gcttcgcat tgaggacggc
1080

ttcagtttga aggagcagct gcaagacatg ggccttgctg atctgttcag cctgaaaag
1140

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1200

cataaggcat ttcttgaggt aatgaagaa ggcagtgaag cagctgcaag taccgctggt
1260

gtgattgctg gccgttcgct aaacccaac agggtgactt tcaaggccaa caggccttcc
1320

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1380

ccttgtgtta agtaa
1395

<210> 64
<211> 464
<212> PRT
<213> Homo sapiens

<400> 64
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Tyr Leu Leu Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys
20 25 30

His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
35 40 45

Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
50 55 60

Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
65 70 75 80

Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
85 90 95

His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
100 105 110

Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
115 120 125

Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
130 135 140

Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
145 150 155 160

Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
165 170 175

Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
180 185 190

Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
195 200 205

Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
210 215 220

Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
225 230 235 240

Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
245 250 255

Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
260 265 270

Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
275 280 285

Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
290 295 300

Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
305 310 315 320

Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
325 330 335

Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
340 345 350

Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
355 360 365

Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
370 375 380

Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
385 390 395 400

His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
405 410 415

Ser Thr Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg Val
420 425 430

Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
435 440 445

Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
450 455 460

<210> 65

<211> 1962

<212> DNA

<213> Homo sapiens

<400> 65

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120

tggccctgc ggcgttctg gaggagcaca ggcttctgcc ccccgctgcc acacagccag
180

gctgaccagt acgtctcag ctgggaccag cagctcaacc tcgcotatgt gggcgccgtg
240

cctcacgcg gcataagca ggtccggacc cactggctgc tggagcttgt caccaccagg
300

gggtccactg gacggggcct gagctacaac ttcacccacc tggacgggta cttggacctt
360

ctcagggaga accagctcct cccaggggtt gagctgatgg gcagcgccctc gggccaattc
420

actgactttg aggacaagca gcaggtgttt gagggaagg acttggctctc cagcctggcg
480

aggagataca tcggtaggta cggactggcg catgtttcca agtggaaatt cgagacgtgg
540

aatgagccag accaccaga ctttgacaac gtctccatga ccatacgaagg cttcctgaac
600

tactacgatg cctgctcgga gggctctgcg gccgccagcc ccgcctcgcg gctgggaggg
660

cccgcgact ccttcaaac cccacgcga tccccgtga gctggggcct cctgcgccac
720

tgccacagc gtaccaactt cttaactggg gaggcggcg tgcggtgga ctacatctcc
780

ctccacagga agggctcgcg cagctccatc tccatcctgg agcaggagaa ggtcgtcgcg
840

cagcagatcc ggcagctctt cccaagttc ggggacacc ccatttcaa cgacgagggg
900

gaccgcgtgg tgggctggtc cctgccacag ccgtggaggg cggacgtgac ctacgcggcc
960

atggtggtga aggtcatcgc gcagcatcag aacctgctac tggccaacac cacctccggc
1020

ttccctacg cgctcctgag caacgacaat gccttctga gctaccaccc gcacccttc
1080

ggcagcgca cgtcacccg gcgcttcag gtcaacaaca cccgcccgcc gcagtgagc
1140

ctgttcgca agccggtgct caccggcatg gggctgctgg cgtgctgga tgaggagcag
1200

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1260

ctggccagcg cccacagccc ccagggcccg gccgacgcct ggcgcgcgc ggtgctgac
1320

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1380

cgcggggtgc cccccggccc gggcctggtc tacgtcacgc gctacctgga caacgggctc
1440

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1500

tccggcgca tgcgcgcgcg tgaggaccog gtggcgcgcg cgcgccccc cttaccgcgc
1560

ggcgccccc tgacctgcg cccgcgcctg cggctgcct cgcttttct ggtgcacgtg
1620

tgtgcgcgc cagagaagcc gccggggcag gtcacgcgcg tcgcgcctt gccctgacc
1680

caagggcagc tggttctggt ctggtcgat gaacacgtg gctccaagt cctgtggaca
1740

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1800

acctoaacc tctttgtgtt cagcccagac acaggtgctg tctctggctc ctaccgagtt
1860

cgagccctgg actactgggc ccgaccaggc cccttctcgg accctgtgcc gtacctggag
1920

gtccctgtgc caagagggcc cccatcccg ggcaatccat ga
1962

<210> 66

<211> 653

<212> PRT

<213> Homo sapiens

<400> 66

Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser
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Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
20 25 30

Gln Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
35 40 45

Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
50 55 60

Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
65 70 75 80

Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
85 90 95

Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr

100										105										110											
His	Leu	Asp	Gly	Tyr	Leu	Asp	Leu	Leu	Arg	Glu	Asn	Gln	Leu	Leu	Pro																
115										120										125											
Gly	Phe	Glu	Leu	Met	Gly	Ser	Ala	Ser	Gly	His	Phe	Thr	Asp	Phe	Glu																
130										135										140											
Asp	Lys	Gln	Gln	Val	Phe	Glu	Trp	Lys	Asp	Leu	Val	Ser	Ser	Leu	Ala																
145										150										155											
Arg	Arg	Tyr	Ile	Gly	Arg	Tyr	Gly	Leu	Ala	His	Val	Ser	Lys	Trp	Asn																
165										170										175											
Phe	Glu	Thr	Trp	Asn	Glu	Pro	Asp	His	His	Asp	Phe	Asp	Asn	Val	Ser																
180										185										190											
Met	Thr	Met	Gln	Gly	Phe	Leu	Asn	Tyr	Tyr	Asp	Ala	Cys	Ser	Glu	Gly																
195										200										205											
Leu	Arg	Ala	Ala	Ser	Pro	Ala	Leu	Arg	Leu	Gly	Gly	Pro	Gly	Asp	Ser																
210										215										220											
Phe	His	Thr	Pro	Pro	Arg	Ser	Pro	Leu	Ser	Trp	Gly	Leu	Leu	Arg	His																
225										230										235											
Cys	His	Asp	Gly	Thr	Asn	Phe	Phe	Thr	Gly	Glu	Ala	Gly	Val	Arg	Leu																
245										250										255											
Asp	Tyr	Ile	Ser	Leu	His	Arg	Lys	Gly	Ala	Arg	Ser	Ser	Ile	Ser	Ile																
260										265										270											
Leu	Glu	Gln	Glu	Lys	Val	Val	Ala	Gln	Gln	Ile	Arg	Gln	Leu	Phe	Pro																
275										280										285											
Lys	Phe	Ala	Asp	Thr	Pro	Ile	Tyr	Asn	Asp	Glu	Ala	Asp	Pro	Leu	Val																
290										295										300											
Gly	Trp	Ser	Leu	Pro	Gln	Pro	Trp	Arg	Ala	Asp	Val	Thr	Tyr	Ala	Ala																
305										310										315											
Met	Val	Val	Lys	Val	Ile	Ala	Gln	His	Gln	Asn	Leu	Leu	Leu	Ala	Asn																
325										330										335											
Thr	Thr	Ser	Ala	Phe	Pro	Tyr	Ala	Leu	Leu	Ser	Asn	Asp	Asn	Ala	Phe																
340										345										350											
Leu	Ser	Tyr	His	Pro	His	Pro	Phe	Ala	Gln	Arg	Thr	Leu	Thr	Ala	Arg																
355										360										365											
Phe	Gln	Val	Asn	Asn	Thr	Arg	Pro	Pro	His	Val	Gln	Leu	Leu	Arg	Lys																
370										375										380											
Pro	Val	Leu	Thr	Ala	Met	Gly	Leu	Leu	Ala	Leu	Leu	Asp	Glu	Gln	Gln																
385										390										395											
Leu	Trp	Ala	Glu	Val	Ser	Gln	Ala	Gly	Thr	Val	Leu	Asp	Ser	Asn	His																
405										410										415											
Thr	Val	Gly	Val	Leu	Ala	Ser	Ala	His	Arg	Pro	Gln	Gly	Pro	Ala	Asp																
420										425										430											

Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
 435 440 445

His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro
 450 455 460

Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
 465 470 475 480

Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
 485 490 495

Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
 500 505 510

Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
 515 520 525

Ala Leu Arg Leu Pro Ser Leu Leu Val His Val Cys Ala Arg Pro
 530 535 540

Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr
 545 550 555 560

Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys
 565 570 575

Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr
 580 585 590

Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
 595 600 605

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp
 610 615 620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
 625 630 635 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
 645 650

<210> 67

<211> 1290

<212> DNA

<213> Homo sapiens

<400> 67

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 120

accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgccca ggaagagcca
 180

gattcctgca tcagtgagaa gctcttcacg gagatggcag agctcatggt ctcagaaggc
 240

tggaaggatg cagggttatga gtacctctgc attgatgact gttggatggc tccccaaga
300

gattcagaag gcagacttca ggcagacctc cagcgcttcc ctcatgggat tcgccagcta
360

gctaattatg ttacacagaa aggactgaag ctagggtatt atgcagatgt tggaaataaa
420

acctgcgcag gcttccctgg gagttttgga tactacgaca ttgatccca gacctttgct
480

gactggggag tagatctgct aaaatttgat ggttggtact gtgacagttt ggaaaatttg
540

gcagatgggt ataagcacat gtccctggcc ctgaatagga ctggcagaag cattgtgtac
600

tcctgtgagt ggccctctta tatgtggccc ttcaaaagc ccaattatac agaaatccga
660

cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag
720

agtatcttgg actggacatc ttttaaccag gagagaattg ttgatgttgc tggaccaggg
780

ggttggaatg acccagatat gttagtgtt ggcaactttg gcctcagctg gaatcagcaa
840

gtaactcaga tggccctctg ggctatcatg gctgctcctt tattcatgtc taatgacctc
900

cgacacatca gccctcaagc caaagctctc cttcaggata aggacgtaat tggcatcaat
960

caggacctct tgggcaagca aggttaccag cttagacagg gagacaactt tgaagtgtgg
1020

gaacgacctc tctcaggctt agcctgggct gtacttatga taaaccggca ggagatttgt
1080

ggacctgctg cttataccat cgcagttgct tccctgggta aaggagtggc ctgtaatcct
1140

gcctgcttca tcacacagct cctccctgtg aaaaggaagc tagggttcta tgaatggact
1200

tcaaggttaa gaagtcacat aaatcccaca ggcactgttt tgcttcagct agaaaataca
1260

atgcagatgt cattaaaaga cttactttaa
1290

<210> 68

<211> 429

<212> PRT

<213> Homo sapiens

<400> 68

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu

Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
 20 25 30
 Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45
 Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
 50 55 60
 Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
 65 70 75 80
 Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
 85 90 95
 Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
 100 105 110
 Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
 115 120 125
 Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
 130 135 140
 Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
 145 150 155 160
 Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
 165 170 175
 Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
 180 185 190
 Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
 195 200 205
 Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
 210 215 220
 His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys
 225 230 235 240
 Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
 245 250 255
 Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
 260 265 270
 Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
 275 280 285
 Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
 290 295 300
 Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
 305 310 315 320
 Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
 325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
 340 345 350
 Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
 355 360 365
 Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
 370 375 380
 Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
 385 390 395 400
 Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
 405 410 415
 Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu
 420 425

<210> 69
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 69
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 120

ttcttctccc agccgggtgc cccaatactt cagtgcattg gctgctgctt ctctagagca
 180

tatccactc cactaaggtc caagaagacg atgttggtcc aaaagaacgt cacctcagag
 240

tccacttgct gtgtagctaa atcatataac agggtcacag taatgggggg ttccaaagt
 300

gagaaccaca cggcgtgcca ctgcagtact tgttattatc acaaatotta a
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<210> 70
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 70
 Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
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Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
 20 25 30

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
 35 40 45

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
 50 55 60

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
65 70 75 80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
85 90 95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
100 105 110

Tyr His Lys Ser
115

<210> 71

<211> 498

<212> DNA

<213> Homo sapiens

<400> 71

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120

gagggctgcc ccgtgtgcat caccgtcaac accaccatct gtgcgggcta ctgcccacc
180

atgacccgcg tgctgcaggg ggtcctgccg gccctgcctc aggtggtgtg caactaccg
240

gatgtgogct tcgagtccat ccggtccct ggctgccgc gcggcgtgaa ccccggtgc
300

tcctacggcg tggctctcag ctgtcaatgt gcactctgcc gcgcagcac cactgactgc
360

gggggtccca aggaccacc ctgacctgt gatgacccc gcttcaggga ctctcttcc
420

tcaaaggccc ctccccccag ccttccaagc ccattccgac tccgggggcc ctggacacc
480

ccgatactcc cacaataa
498

<210> 72

<211> 165

<212> PRT

<213> Homo sapiens

<400> 72

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Ser Met Gly
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Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile
20 25 30

Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr
35 40 45

Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val

50

55

60

Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg
65 70 75 80

Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val
85 90 95

Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu
100 105 110

Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu
115 120 125

Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro
130 135 140

Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr
145 150 155 160

Pro Ile Leu Pro Gln
165

<210> 73

<211> 165

<212> PRT

<213> Homo sapiens

<400> 73

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
1 5 10 15

Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
20 25 30

Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
35 40 45

Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
50 55 60

Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
65 70 75 80

Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
85 90 95

Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
100 105 110

Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
115 120 125

Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
130 135 140

Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
145 150 155 160

Cys Arg Thr Gly Asp
165

<210> 74
 <211> 588
 <212> DNA
 <213> Homo sapiens

<400> 74
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tctctgggct gtgatctgcc tcagaacctt ggccacttta gcaggaacac cttgggtgctt
 120

ctgcacaaaa tgaggagaat ctcccctttc ttgtgtctca aggacagaag agacttcagg
 180

ttccccccagg agatggtaaa agggagccag ttgcagaagg cccatgtcat gtctgtcctc
 240

catgagatgc tgcagcagat cttcagcctc ttccacacag agcgctcctc tgetgctctg
 300

aacatgaccc tcttagacca actccacact ggacttcac agcaactgca acacctggag
 360

acctgcttgc tgcaggtagt gggagaagga gaatctgctg ggcaattag cagccctgca
 420

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Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
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Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
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His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
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Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu
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 His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
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 Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg
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 Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser
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 Gly Ser Ser
 195

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